

# SEARCH REQUEST FORM

Requestor's

Name: Sally Teng

Serial

Number: 08/455,682

Date: 7/22/97

Phone: 302-4230

Art Unit: 1812

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

- (1) Please search SEQ ID NO. 1-4, 11, 12
- (2) Search ligand for opioid receptor
- (3) Search ligand for chimeric opioid recept.

08/292694

05/31/95

OPIOID RECEPTORS; COMPOSITIONS AND METHODS

BELL, GRAEME I,

## STAFF USE ONLY

Date completed: 8-26-97

Searcher: MARK

Terminal time: 65

Elapsed time: prop 5

CPU time: \_\_\_\_\_

Total time: 70

Number of Searches: 1

Number of Databases: 7

### Search Site

☐ STIC

☒ CM-1

☐ Pre-S

### Type of Search

☒ N.A. Sequence

☒ A.A. Sequence

☐ Structure

☐ Bibliographic

### Vendors MPRCH

☒ IG

☐ STN

☐ Dialog

☐ APS

☐ Geninfo

☐ SDC

☐ DARC/Questel

☐ Other

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JOURNAL Biochem. Biophys. Res. Commun. 202 (3), 1431-1437 (1994)  
MEDLINE 94338360  
REFERENCE 3 (bases 1 to 1154)  
AUTHORS Kieffer,B.  
TITLE Direct Submission  
JOURNAL Submitted (18-NOV-1994) Brigitte Kieffer, Ecole Supérieure De  
Biotechnologie De Strasbourg, Boulevard Sebastien Brandt, Ilkirch,  
67400, France

FEATURES  
Source location/Qualifiers  
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DEFINITION Homo sapiens (clone d2-115) kappa opioid receptor (OPRK1) mRNA,  
complete cds.  
ACCESSION L37362  
NID 9722617  
KEYWORDS OPRK1 gene; kappa opioid receptor; opioid receptor;  
SOURCE Homo sapiens (clone d2-115) (tissue library: genomic in lambda dash  
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ORGANISM Homo sapiens  
Eukaryoteae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1604)  
AUTHORS Zhu,J., Chen,C., Xue,J.-C., Kunapuli,S., Deriel,J.K. and  
Liu-Chen,L.-Y.  
TITLE Cloning of a human .kappa. opioid receptor from the brain  
JOURNAL Life Sci. 56, 201-207 (1995)  
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Best Local Similarity 98.4%; Pred. No. 0.00e+00;  
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DEFINITION Human kappa opioid receptor (hKOR) mRNA, complete cds.  
ACCESSION U11053  
NID 9532059  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

REFERENCE  
1 (bases 1 to 1182)  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
REFERENCE  
2 (bases 1 to 1182)  
AUTHORS  
TITLE  
JOURNAL  
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QY 1000 A 1000

RESULT 4 CPU04092 1733 bp mRNA ROD 24-MAY-1995

LOCUS Cavia porcellus Hartley kappa opioid receptor mRNA, complete cds.

DEFINITION U04092

ACCESSION 9476106

NID

KEYWORDS

SOURCE

ORGANISM

guinea pig.

Cavia porcellus

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Rodentia; Hystriocognathi; Cavidae; Cavia.

REFERENCE

1 (bases 1 to 1733)

Xie,G.X., Meng,F., Mansour,A., Thompson,R.C., Hoversten,M.T., Goldstein,A., Watson,S.J. and Akil,H.

Primary structure and functional expression of a guinea pig kappa opioid (dynorphin) receptor

Proc. Natl. Acad. Sci. U.S.A. 91 (9), 3779-3783 (1994)

94224825

JOURNAL

2 (bases 1 to 1733)

REFERENCE

Xie,G.

Direct Submission

Submitted (07-DEC-1993) Guo-xi Xie, Mental Health Research Institute, The University of Michigan, 205 Zina Pitcher Place, Ann Arbor, MI 48109-0720, USA

JOURNAL

Location/Qualifiers

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Best Local Similarity 89.5%; Pred. No. 0.00e+00;

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QY 159 GCTTTAGTTACTACAACCATGCCCTTTACAGAGTACGGTCTACTTGAATGAATTCCTGGCCT 218

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ACCESSION	L11065		
NID	9348248		
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ORGANISM	Mus musculus		
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 1410) Yasuda,K., Raynor,K., Kong,H., Breder,C.D., Takeda,J., Reisine,T. and Bell,G.I.		
TITLE	Cloning and functional comparison of kappa and delta opioid receptors from mouse brain		
JOURNAL MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 90, 6736-6740 (1993)		
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	LVVAVFICWPIHIFILVEALGSTSHSTALSSYFICIALGYNNSINPVLVYAFLD		
	ENFKRCFRDFCFPIKMMERQSTNRVRNTVQDPASMRDVGGMKPY"		
BASE COUNT	322 a	360 c	337 g 391 t
ORIGIN			

Query Match 67.4%; Score 670; DB 89; Length 1410;  
Best Local Similarity 87.7%; Pred. No. 0.00e+00;  
Matches 790; Conservative 0; Mismatches 108; Indels 3; Gaps 2;

Db	442	gatacacgaagatgaagaccgcaaccaacatctacataattaacctggttggcagatg	501
QY	100	GATACACAAAGATGAAGACAGCAACCAATTTACATATTAACTGGCTTTGGCAGATG	159
Db	502	cttggttactaccactatgccccttcagagtgtgtctacttgatgaattctggccctt	561
QY	160	CTTTAGTTACTACAAACCATGGCCTTTCAGAGTACGGTCTACTGATGAATTCCTGGCCTT	219
Db	562	ttggagatgtgtctatgcaagattgttcatttcattgactactacaacatgtttaccagca	621
QY	220	TTGGGGATGTGCTGTGCAAGATAGTAATTTCCATGTGATTACTACAACATGTTCACACGCA	279
Db	622	tattcaaccttgaccatgatgatgtgtggaccgctacattgtgtgtgccaccctgtgaag	681
QY	280	TCTTCACCTTGACCATGATGAGCGGTGGACCGCTACATTTGCCGTGTGCCACCCCGTGAAG	339
Db	682	ctttggacctccgaacacctttgaaagaagatcatcaacatctgcatttggctcctgg	741
QY	340	CTTTGGACCTTCGGCACACCCTTGAAGGCAAGATCATCAATATCTGCATCTGGCTGTGT	399
Db	742	catcatctgttgytatatacagcgatagtccttggagaccacaaagtcaggygaagtgyg	801
QY	400	CGTCATCTGTGGCATCTCTGCATACTAGTCCTTGGAGGCACCAAAAGTCAGGGAAGTGTG	459
Db	802	atgtcaattgaatgctcctcttgcaagtttcctgtatgatgaatatcctggtggagatctctca	861
QY	460	ATGTCAATTGAGTGTGCTGTGCATTCCTTCGTGATCCCTGTCTCATCATCATCGTCTGCTCA	519
Db	862	tgaagatctgtgtcttctgtcttggccttgtgtatcccaagtcctcatcatcatltgtctgt	921
QY	520	TGAAGATCTGCGTCTTCATCTTTCCTTCGTGATCCCTGTCTCATCATCATCGTCTGCT	579
Db	922	acacacctgatgatcctctggccctcaagaagtgtccggtcctctctgtctcccgagagaag	981
QY	580	ACACCTGATGATCTCTGCGCTCTCAAGANNGTCCGGCTCTTCTGTGGCTCCCGAGAGAAAG	639
Db	982	accgaaatctccgcgcgcataccaacgtgtgtgtgtagtagttgcagtcctcatcatct	1041
QY	640	ATTNCAACCTGCGTAGGATCACCAACTGGTCTGTGTGGTGGTGGCAGTCTTCGTCTGCT	699
Db	1042	gttggaccgcccatctacatcttatacctgtgtggaagctcttgggaagcacctccacagca	1101
QY	700	GCTGACTGCCCATTCACATATTCATCTGCTGTGGAGGCTCTGGGGAGCACCTCCACAGCA	759
Db	1102	cagctgcccctccocaactattatctgtattgttgcccttgggttataccaacagcagctga	1161
QY	760	CAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTATACCAACAGTAGCCTGA	819
Db	1162	atcctgttctctatagccttctctgtgataaacttcaagcggtgttttagggacttctgtct	1221
QY	820	ATCCCATTTCTCTACGCCCTTTCTTGATCAAAACTTCAAGCGGTGTTCGGGACTTCTGCT	879
Db	1222	tcacctattaagatgcgaatggaagcgccagagcaaccaatagagtttagaaacacagttcaag	1281
QY	880	TTCCACTGAAGATGAGNATGGAGCGGCNAGACACTAGCAGAGTCCGAATAATACAGTTCAGG	939
Db	1282	atcctgtcttccatgag--agat-gtggagggatgtaataagccagtatgactagtctgg	1338
QY	940	ATCCTGCTTAACCTGAGGGAGATCGATGGATGATTAACACAGTATGACTAGTGTGG	999
Db	1339	a 1339	
QY	1000	A 1000	

RESULT 7  
LOCUS RATRORD 1273 bp mRNA ROD 21-DEC-1993  
DEFINITION Rat mRNA for opioid receptor, complete cds.  
ACCESSION D16534

NID g409390  
KEYWORDS G-protein coupled receptor; opioid receptor; transmembrane protein.  
SOURCE Rattus norvegicus (strain Wistar) adult brain cDNA to mRNA, clone pROR2.

ORGANISM Rattus norvegicus  
Eukaryota; Eukarya; Chordata; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 1273)  
AUTHORS Nishi,M., Takeshima,H., Fukuda,K., Kato,S. and Mori,K.  
TITLE cDNA cloning and pharmacological characterization of an opioid receptor with high affinities for .kappa.-subtype-selective ligands  
JOURNAL FEBS Lett. 330, 77-80 (1993)  
MEDLINE 93380575  
COMMENT Submitted (19-JUN-1993) to DBJ by: Hiroshi Takeshima  
International Institute  
for Advanced Studies  
c/o Shimadzu Corporation  
N-80  
1 Nishinokyo-Kuwahara-cho  
Kyoto 604  
Japan  
Phone: 075-823-1208  
Fax: 075-811-8186.

FEATURES  
source Location/Qualifiers  
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CDS  
BASE COUNT 278 a 340 c 294 g 361 t  
ORIGIN

Query Match 66.6%; Score 662; DB 91; Length 1273;  
Best Local Similarity 87.2%; Pred. No. 0.00e+00;  
Matches 786; Conservative 0; Mismatches 112; Indels 3; Gaps 1;

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QY	100	GATACACAAAGATGAAGACAGCAACCAACATTACATATTTAACCTGGCTTGGCAGATG	159
Db	365	cttggttactaacactatgcccctccagagtgctgtctacttgatgaattcttggcctt	424
QY	160	CTTTAGTTACTACAACCATGGCCTTTCAGAGTACGGTCTACTTGATGAATTCTGGCCTT	219
Db	425	ttggagatgtctgtgcaagattgtcatlttccattgactactacaacatgtttaccagca	484
QY	220	TTGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAACATGTTCAACAGCA	279
Db	485	tattcaaccttgaccatgatgagtggaccgctacattgcccgtgtgccaccctgtgaag	544
QY	280	TCTTCACCTTGACCATGATGAGCGGTGACCGCTACATTGGCGTGTGCCACCCCGTGAAG	339
Db	545	cttggatttccgaacacctttgaaagcaagatcatcaacatctgcatttggctactgg	604
QY	340	CTTTGACTTCCGCACACACCTTGAAGCAAGATCATCAATATCTGCATCTGGCTGTGT	399
Db	605	catcatctgttggatatatacagcgatagtccttggagggacccaagtcaaggaagtgtg	664
QY	400	CGTCATCTGTTGGCATCTCTGCATAATAGTCTTGGAGGCAACCAAAAGTCAAGGAAGTGTG	459



Db	665	atgtcattgaatgctcccttcgaagtttcctgatgatgaatatctcgttggaccctctca	724
QY <td>460</td> <td>ATGTCAATTGAGTGCCTGCTTGGCAATTCOCAGATGATGACTACTCCCTGGATGGACCTCTTCA</td> <td>519</td>	460	ATGTCAATTGAGTGCCTGCTTGGCAATTCOCAGATGATGACTACTCCCTGGATGGACCTCTTCA	519
Db <td>725</td> <td>tgaagatcgtgtctcgtcttcgtcccttgtttatccctgtctcraatcatcatlgtctgct</td> <td>784</td>	725	tgaagatcgtgtctcgtcttcgtcccttgtttatccctgtctcraatcatcatlgtctgct	784
QY <td>520</td> <td>TGAAGATCTGGCGTCTTCATCTTTGCCCTTCGTGATCCCTGCTCCTCATCATCATGCTCTGCT</td> <td>579</td>	520	TGAAGATCTGGCGTCTTCATCTTTGCCCTTCGTGATCCCTGCTCCTCATCATCATGCTCTGCT	579
Db <td>785</td> <td>acacccctgatgatcctcgtcgttgaagaagtgtccggtccctcgtgggtctcogagaagaag</td> <td>844</td>	785	acacccctgatgatcctcgtcgttgaagaagtgtccggtccctcgtgggtctcogagaagaag	844
QY <td>580</td> <td>ACACCCCTGATGATCTCGCTTCAGATTCAGANNGTCCGGCTCCTTCTGGCTCCCGAGAGAAAG</td> <td>639</td>	580	ACACCCCTGATGATCTCGCTTCAGATTCAGANNGTCCGGCTCCTTCTGGCTCCCGAGAGAAAG	639
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QY <td>640</td> <td>ATTNCAACCTGGCTAGGATCACACAGACTGGTCCCTGGTGGTGGGAGACTCTTGGCTCT</td> <td>699</td>	640	ATTNCAACCTGGCTAGGATCACACAGACTGGTCCCTGGTGGTGGGAGACTCTTGGCTCT	699
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QY <td>700</td> <td>GCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGGAGCACTCCACAGACA</td> <td>759</td>	700	GCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGGAGCACTCCACAGACA	759
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QY <td>760</td> <td>CAGCTGCTCTCTCCAGCTATTACTTCTGTCATGCGCTTAGGCTATTACCAACAGTAGCCTGA</td> <td>819</td>	760	CAGCTGCTCTCTCCAGCTATTACTTCTGTCATGCGCTTAGGCTATTACCAACAGTAGCCTGA	819
Db <td>1025</td> <td>atcctgttctctatgaccttcttgatgaaacctcaagcgggttttagggactctgct</td> <td>1084</td>	1025	atcctgttctctatgaccttcttgatgaaacctcaagcgggttttagggactctgct	1084
QY <td>820</td> <td>ATCCCATTTCTTACGCGCTTTCTTGATGAAAACTTCAAGCGGTGTTCCGGGACTTCTGCT</td> <td>879</td>	820	ATCCCATTTCTTACGCGCTTTCTTGATGAAAACTTCAAGCGGTGTTCCGGGACTTCTGCT	879
Db <td>1085</td> <td>tcccatcctaagatgcgaatggagcgccagagcacacaacagagttagaacacagttcagg</td> <td>1144</td>	1085	tcccatcctaagatgcgaatggagcgccagagcacacaacagagttagaacacagttcagg	1144
QY <td>880</td> <td>TTCCACTGAAGATGAGNATGGAGCGGCNAGAGCACTAGCAGATCCGAATACAGTTCCAGG</td> <td>939</td>	880	TTCCACTGAAGATGAGNATGGAGCGGCNAGAGCACTAGCAGATCCGAATACAGTTCCAGG	939
Db <td>1145</td> <td>atcctgtctccatgagagatgtgtgtgtggtgga--ataagccagttatgactagtcatg</td> <td>1201</td>	1145	atcctgtctccatgagagatgtgtgtgtggtgga--ataagccagttatgactagtcatg	1201
QY <td>940</td> <td>ATCCTGCTTACCTGAGGAGATCGATGGATGATGAATAAACAGTATGACTAGTCTGTGG</td> <td>999</td>	940	ATCCTGCTTACCTGAGGAGATCGATGGATGATGAATAAACAGTATGACTAGTCTGTGG	999
Db <td>1202</td> <td>a 1202</td> <td></td>	1202	a 1202	
QY <td>1000</td> <td>A 1000</td> <td></td>	1000	A 1000	

RESULT	8			
LOCUS	RATKOR1A	1358 bp	mRNA	ROD
DEFINITION	Rat kappa opioid receptor mRNA, complete cds.			21-OCT-1993
ACCESSION	L22001			
NID	9409236			
KEYWORDS	kappa opioid receptor; opioid receptor.			
SOURCE	Rattus norvegicus whole brain cDNA to mRNA.			
ORGANISM	Rattus norvegicus			
	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.			
REFERENCE	1 (bases 1 to 1358)			
AUTHORS	Chen, Y., Mestek, A., Liu, J. and Yu, L.			
TITLE	Molecular cloning of a rat kappa opioid receptor reveals sequence similarities to the mu and delta opioid receptors			
JOURNAL	Biochem. J. 295, 625-628 (1993)			
MEDLINE	94059008			
FEATURES				
source	Location/Qualifiers			
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	LADALVTMTFQSAVYIMNSWPEGLVKIVISIDYNNFTSIFLTMSVDRIAY			
	CHPVKALDFRTPKAKIINICIMWLASSVGISAIVLGGTKREDVDVIECSIQPDE			
	YSWMDLEMKICEVFVAFVIVLIIYGYTIMLRKSVRLSGSREKDRNLRITKIV			
	LVVAVFIIICWTPIHIFILFIVEALGTSHTAVLSISYFICIALGYTNSLNPLYAFLD			

BASE COUNT	304 a	353 c	320 g	381 t	ENFKRCRDFCFPIKMRMERQSTNRYVNTVQDPASMRDVGKMKPV"
Query Match					66.6%; Score 662; DB 90; Length 1358;
Best Local Similarity					87.2%; Pred. No. 0.00e+00;
Matches					786; Conservative 0; Mismatches 112; Indels 3; Gaps 1;
Db	327	gatacacaagaatgaagacgcgaaccaacatctacatatttaacctggtcttgccagatg			386
QY	100	GATACACAAGATGAAGACACCAACCAACATTTACATATTTAACTGGCTTTGGCAGATG			159
Db	387	cttgggttactaccactatgccccctccagagtgtgtctacttgaatcttgccctt			446
QY	160	CTTTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTGATGAATTCCGTGCCCTT			219
Db	447	ttggagatgttctgtgcaagaattgtcatttccattgactactacaacatggtttaccagca			506
QY	220	TTGGGATGTGCTGTGCAAGATAGTAATTTCATGTGATTACTACAACATGTTCACCAGCA			279
Db	507	tattcaccttgacacatgtagtgtgagccgctacattgcccgtgtgcccaccctgtgaaag			566
QY	280	TCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGTGCCACCCCGTGAAG			339
Db	567	cttggattcccgacacacotttgaaagcaagaatcatcaacatctgcatttggctactg			626
QY	340	CTTTGGACTCCGACACACCCCTTGAAGGCAAGATCATCAITATCTGCATCTGGCTGTGT			399
Db	627	catcatctgttgtatatacagcgatagtccttggaggcaccaaagtcaaggaaagtgtg			686
QY	400	CGTCATCTGTTGGCATCTCTGCATATAGTCCCTTGGAGGCCAACAAAGTCAGGGAAGTGTG			459
Db	687	atgtcatatgaatgctcccttgcaagttccctgatgatgaatatctcgtgtgagcccttca			746
QY	460	ATGTCAITGAGTGTGCTTGGAGTCCAGATGATGACTACTCCTGTGTGGAGCCCTGTCA			519
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QY	520	TGAAGATCTGCGTCTTCACTTTGGCCTTCGTGATCCCTGTCCCTCATCATCATCTGTCT			579
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QY	580	ACACCCGTATGATCTCTGCGTCTCAAGANNGTCCGGCTCTTCTGTGCTCCCGAGGAAG			639
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QY	640	ATNNCAACCTGCGTAGGATCAACAGACTGTCTGTGTGTGTGGCAGTCTTGTGTCT			699
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QY	700	GCTGGACTCCCATTCACATATTCATCCTGTGTGGAGGCTCTGGGGAGCACCTCCACAGCA			759
Db	987	cagctgtccctctctagctattactctctgcattgccccttgggttataccaacagcagcttga			1046
QY	760	CAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTATACCAACAGTAGCCTGA			819
Db	1047	atcctgttctctatgaccttcttcttgatgaaaactcaagcggtgtttaggaaactctgct			1106
QY	820	ATCCCATCTCTTACGGCCTTCTTGATGAATAACTTCAAGCGGTGTTCCGGGACTTCTGCT			879
Db	1107	tcccacattaagatgcgaatgagcgccagagcacaaacagagttagaacacagttcagg			1166
QY	880	TTCCACTGAAGATGAGNATGGAGCGGNAGAGCACTAGCAGAGTCCGAATACAGTTCCAGG			939
Db	1167	atccgtcttccatgagggaatgtgtgtggtatga--ataagccagtatgactagtcatgg			1223
QY	940	ATCCTGCTTACCTGAGGAGATCGATGGGATGATGAATAAACCAAGTATGACTAGTGTGG			999
Db	1224	a 1224			
QY	1000	A 1000			

[illegible]

LOCUS	10	RATKOR	2481 bp	MRNA	ROD	02-DEC-1993
DEFINITION		Rattus norvegicus	mrna	for kappa opioid receptor, complete cds.		
ACCESSION		D16829				
NID		g404115				
KEYWORDS		kappa opioid receptor.				
SOURCE		Rattus norvegicus		CDNA to mRNA.		
ORGANISM		Rattus norvegicus				
REFERENCE		1 (bases 1 to 2481)				
AUTHORS		Minami,M., Toya,T., Katao,Y., Maekawa,K., Nakamura,S., Onogi,T., Kaneko,S. and Satoh,M.				
TITLE		Cloning and expression of a cDNA for the rat kappa-opioid receptor				
JOURNAL		FEBS Letters 329, 291-295 (1993)				
MEDLINE		93374033				
COMMENT		Submitted (21-JUN-1993) to DDBJ by: Masabumi Minami				
		Department of Pharmacology				
		Faculty of Pharmaceutical Sciences				
		Kyoto University				
		Kyoto, Kyoto 606-01				
		Japan				
		Phone: 075-753-4546				
		Fax: 075-753-4586.				
FEATURES		Location/Qualifiers				
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Db	753	ctctgcatcttcocgaacacaccttgaagcagaatcatcaacatctgtactgtg	812
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Db	813	catcatctgttggtatatacagcgatagtccttggaggcaccocaaagtcaaggagatgtgg	872
QY	400	CGTCACTGTGGGCATCTCTGCAATAGTCTTTGGAGGCACCAAAAGTCAAGGGAAGGTGCG	459
Db	873	atgtcatlgaatgcctccttgcagttccctgatgatgaalatcctgtgtggacctctca	932
QY	460	ATGTCAATTGAGTGTGCTTGAGTCCAGTCCAGATGATGACTACTCCTGTGTGGACCTCTTCA	519
Db	933	tgaagatctgtgtcttcgtcttctgtcccttgtatccctgtcttaatcatcatgtctgct	992
QY	520	AGAAGATCTGGCTCTTCATCTTTGCCCTTGGTATCCCTGTCTCATCATCATCTGCTGT	579
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QY	640	ATNNCAACCTGGGTAGGATCACACAGACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT	699
Db	1113	gttggaccccccatcatatcttlatcctgtgtgaggctctaggcagcacctccacagca	1172
QY	700	GCTGGACTCCCATCATATTCATTCCTGGTGGAGGCTCTGGGAGCACCTCCACAGCA	759
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QY	760	CAGCTGCTCTCTCCAGCTTACTTCTGCATCGCTTAGGCTATACCAACAGTAGCCTGA	819
Db	1233	atcctgttctctatgcctttcttgaatgaacactcaagcgtgttttagggacttctgct	1292
QY	820	ATCCATTTCTCTACGCCCTTCTTGATGAAAACTTCAAGCGGTGTTTCCGGGACTTCTGCT	879
Db	1293	tcoccatltaagatgcgaatggagcgccagagcacaaacagagtagaacaacagttcagg	1352
QY	880	TTCCACTGAAGATGAGNATGGAGCGGNAGAGCACACTAGCAGAGTCCGAATATACAGTTCA	939
Db	1353	atcctgtcttccatgagggatgt	1409
QY	940	ATCCTGCTTACCTGAGGGAGATCGATGGATGATGAATAAACCAAGTATGACTAGTGTGG	999
Db	1410	a 1410	
QY	1000	A 1000	
RESULT	12		
LOCUS	HUMOPRK1A	455 bp	DNA
DEFINITION	Homo sapiens (clone hSR4-1)	kappa opioid receptor (OPR1) gene,	PRI 07-JAN-1995
		complete exon.	
ACCESSION	L26079		
NID	g416143		
KEYWORDS	OPR1 gene; kappa opioid receptor.		
SOURCE	Homo sapiens (tissue library: Stratagene 946203; lambda)	male	
ORGANISM	Homo sapiens		
	Eukaryota; Eukaryotes; Metazoa; Chordata;		
	Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
REFERENCE	1 (bases 1 to 455)		
AUTHORS	Yasuda,K., Espinosa,R.II., Takeda,J., Le Beau,M.M. and Bell,G.I.		
TITLE	Localization of kappa opioid receptor gene to human chromosome band		
JOURNAL	8q11.2		
FEATURES	Unpublished (1994)		
	Location/Qualifiers		
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BASE COUNT	125 a	104 c	96 g	130 t
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Query Match	45.8%; Score 455; DB 82; Length 455;			
Best Local Similarity	100.0%; Pred. No. 0.00e+00;			
Matches	455; Conservative	0; Mismatches	0; Indels	0; Gaps
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Db	61	ttgaaatgaggggaaatgctattgtttctttcttttagatacacaagaatgaacag	120	
QY	61	TTGAAATGGAGGGAATGCTATGTGTTCTTTCTTTTAGATACACAAAGATCAAGACAG	120	
Db	121	caaccaacatttacataatttaacctggtttggcagatgcttttagttactacaacatgc	180	
QY	121	CAACCAACATTTACATATTTTAACCTGGCTTTGGCAGATGCTTTAGTTACTACAAACATGC	180	
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QY	241	TAGTAATTTCCATGTGATTACTACAACATGTTACACAGCATCTTCACCTTGACCATGATGA	300	
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QY	301	GCGTGGACCGCTACATTGGCGGTGTGCCACCCCGTGAAGGCTTTGGACTTCGGCACACCCCT	360	
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RESULT	13	HUNKOR	432 bp	MRNA
LOCUS				
DEFINITION		Homo sapiens kappa opiate receptor mRNA, partial cds.		PRI
ACCESSION		U36130		13-MAR-1995
NID		g598184		
KEYWORDS		kappa opiate receptor.		
SOURCE		Homo sapiens		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS		1 (bases 1 to 432)		
TITLE		Wang, J.B., Johnson, P.S., Wu, J.M., Wang, W.F. and Uhl, G.R.		
JOURNAL		Human kappa opiate receptor second extracellular loop elevates		
MEDLINE		dynorphin's affinity for human mu/kappa chimeras		
FEATURES		J. Biol. Chem. 269 (42), 25966-25969 (1994)		
source		95014415		
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BASE COUNT	88 a	127 c	100 g	117 t
ORIGIN				

Query Match	42.38;	Score 420;	DB 81;	Length 432;
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QY	609	gtccggtcccttctcgtgctcccgagagaaagatinncaacctgctagatcacaccagactg	668
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QY	669	gtccctggtgtg	680

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DEFINITION	kappa oploid receptor [mice, Genomic, 1186 nt, segment 3 of 3].
ACCESSION	S77872
NID	g998531
KEYWORDS	.
SEGMENT	3 of 3
SOURCE	Mus sp.
ORGANISM	Mus sp.
	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 1186)
AUTHORS	Liu,H.C., Lu,S., Augustin,L.B., Felsheim,R.F., Chen,H.C., Ioh,H.H. and Wei,L.N.
TITLE	Cloning and promoter mapping of mouse kappa oploid receptor gene
JOURNAL	Biochem. Biophys. Res. Commun. 209 (2), 639-647 (1995)
MEDLINE	9525163
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI g1bbsq 166539] from the original journal article. This sequence comes from Fig. 2.
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mRNA	join(S77868:919..1894,S77869:371..723,289..>821)
CDS	join(S77868:1638..1894,S77869:371..723,289..821)
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BASE COUNT	310	a	272	c	254	g	350	t
ORIGIN								
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QY	449	ggaagggtgcgatgtcatTTAGTGTGCTTGCGAGTTCACAGATGACTACTCCTGCTG	508					
Db	344	ggatctcttcataagaatctgtctcctcgctcctttgttatcccaagtccatcat	403					
QY	509	GGACCTCTTCATGAAGATCTGCCTTCATCTTGCCCTTCGTGATCCCTGTCCTCAT	568					
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QY	569	CATCGTCTGTACACCCTGATGATCCTGCGTCTCAAGANNGTCCGGCTCCTTCTGCTC	628					
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QY	629	CCGAGAGAAGATTNNCAACTGCGTAGGATCACACAGACTGGTCCGTGGTGGCGAGT	688					
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QY	689	CTTCGTCTGTCTGTGAGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGGA	748					
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QY	869	GGACTTCTGTCTTCCACTGAAGATGAGNATGAGCGCNAGAGCAGCTAGCAGATCC	928					
Db	764	cacagttcagagatcctgcttccatgag--agat-gtgggagggatgaataagccagt	820					
QY	929	TACAGTTACAGATCCTGCTTACCTGAGGGAGATCGATGGATGATGAATAAACCA	988					
Db	821	actagtctgtga	832					
QY	989	ACTAGTCGTGA	1000					
RESULT	15							
LOCUS	MUSMORGP3	638 bp	DNA					
DEFINITION	Mouse MORGD gene for kappa-opioid receptor, exon 3.							
ACCESSION	D31665							
NID	9643595							
KEYWORDS	g-protein associated; kappa opioid receptor; opioid drugs and peptides-binding; transmembrane protein.							
SEGMENT	3 of 3							
SOURCE	Mus musculus (library: phage lambda fixII) DNA.							
ORGANISM	Mus musculus							
REFERENCE	1 (bases 1 to 638)							
AUTHORS	Nishi,M., Takeshima,H., Mori,M., Nakagawara,K. and Takeuchi,T.							
TITLE	Structure and chromosomal mapping of genes for the mouse kappa-opioid receptor and an opioid receptor homologue (MOR-C)							
JOURNAL	Biochem. Biophys. Res. Commun. 205 (2), 1353-1357 (1994)							

MEDLINE 95100967  
COMMENT Submitted (28-May-1994) to DDBJ by:  
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FEATURES  
Source Location/Qualifiers  
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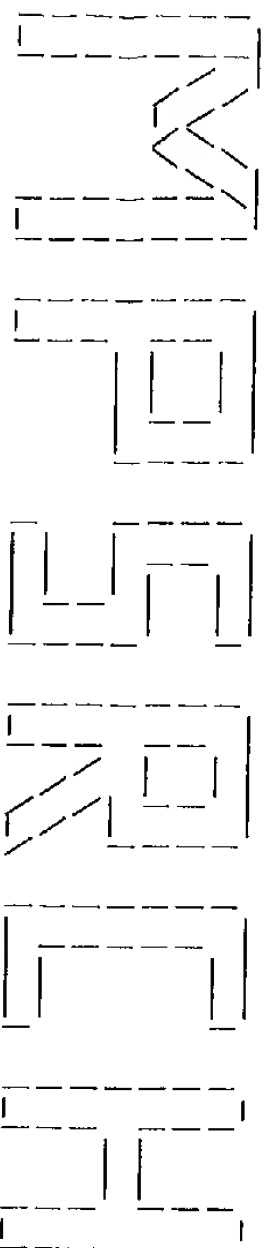
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ORIGIN Chromosome 1 A2-3.

Query Match 38.0%; Score 378; DB 89; Length 638;  
Best Local Similarity 84.9%; Pred. No. 0.00e+00;  
Matches 471; Conservative 0; Mismatches 81; Indels 3; Gaps 2;

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Db 80 gtgggattctctcatgaagatctgtgtgctgctcttgcccttgatcccaagtcctcat 139  
QY 506 GTGGACCTCTTCATGAAGATCTGGCTTCATCTTGCCCTCGTATCCCTGTCTCAT 565  
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QY 566 CATCATGCTGCTGTACACCCGTGATGATCTGGCTCAAGANNGTCCGCTCTTCTGG 625  
Db 200 ctcccgagagaaggaacccaatctccgcgcgcacccaagctgtgtgtgtagtattgc 259  
QY 626 CTCCCGAGAGAAAGATTNNCAACCTGCGTAGGATCACCAAGACTGCTGCTGTTGGC 685  
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QY 686 AGTCTTCGTGCTGTGCTGGAATCCCATACATATTCATCCTGGTGGAGGCTCTGGGAG 745  
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QY 986 ATGACTAGTCGTGGA 1000

Search completed: Tue Aug 26 10:55:10 1997  
Job time : 1231 secs.



(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.  
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Mpsrch\_mn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Aug 26 10:55:32 1997; MasPar time 124.37 Seconds

Tabular output not generated. 791.150 Million cell updates/sec

Title: >US-08-292-694A-11  
Description: (1-1000) from US08292694A.seq  
Perfect Score: 994  
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Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 134151 segs, 49196315 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-geneseq27  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 9.119; Variance 5.514; scale 1.654

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	992	99.8	1000	13	Q75931 Human kappa opioid re	0.00e+00
2	857	86.2	1142	20	T12550 Human kappa opioid re	0.00e+00
3	670	67.4	1410	13	Q75926 Mouse kappa opioid re	0.00e+00
4	660	66.4	2481	15	Q86725 Mammalian kappa opioi	0.00e+00
5	282	28.4	1610	14	Q89226 Human mu opioid recep	2.66e-171
6	282	28.4	2160	15	Q93102 Human mu opiate recep	2.66e-171
7	279	28.1	2070	12	Q79199 Rat mu-subtype opioid	3.27e-169
8	277	27.9	1618	14	Q89222 Human mu opioid recep	8.09e-168
9	277	27.9	1618	14	Q89223 Transcription regulat	8.09e-168
10	265	26.7	1821	10	Q56700 Sequence of murine de	1.81e-159
11	265	26.7	1821	10	Q56705 Partial sequence of t	1.81e-159
12	265	26.7	2272	13	Q75927 Mouse delta opioid re	1.16e-147
13	248	24.9	2216	11	Q66656 Murine delta opioid r	1.40e-145
14	245	24.6	829	10	Q56703 Partial sequence of t	1.40e-145
15	245	24.6	2447	10	Q56702 Partial sequence of t	1.40e-145
16	210	21.1	1567	14	Q89233 Rat opioid receptor c	2.22e-121

17	208	20.9	2706	15	Q92972 Rat opiorph receptor	5.29e-120
18	202	20.3	1330	13	Q75928 Mouse opioid receptor	7.17e-116
19	191	19.2	2600	14	Q90096 Mouse kappa-3 opioid	2.60e-108
20	74	7.4	1047	2	Q10572 Human Natriuretic Pep	4.91e-30
21	73	7.3	1518	14	Q83682 Epsilon opioid recept	2.12e-29
22	70	7.0	1047	2	Q10572 Human Natriuretic Pep	1.69e-27
23	70	7.0	1634	7	Q45653 Human somatostatin re	1.69e-27
24	69	6.9	1265	7	Q45654 Murine somatostatin r	7.23e-27
25	63	6.3	1244	7	Q45656 Pituitary somatostati	4.15e-23
26	61	6.1	1110	5	Q29155 Human somatostatin re	7.24e-22
27	61	6.1	1130	23	T09250 Human somatostatin re	7.24e-22
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30	51	5.1	1796	7	Q45658 Murine somatostatin r	9.15e-16
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32	44	4.4	130	10	Q56701 Partial sequence (seq	1.26e-11
33	43	4.3	91	9	Q51746 Oligonucleotide probe	4.79e-11
34	42	4.2	204	1	N81164 Base substituted E.co	1.81e-10
35	42	4.2	204	1	N81164 Base substituted E.co	1.81e-10
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37	40	4.0	563	9	Q55055 Sequence of orphan re	2.52e-09
38	40	4.0	678	9	Q55056 Generic DNA sequence	9.27e-09
39	39	3.9	114	12	Q70468 Brain somatostatin re	3.38e-08
40	38	3.8	822	5	Q29156 Generic DNA sequence	1.22e-07
41	37	3.7	114	12	Q70466 Generic DNA sequence	4.39e-07
42	36	3.6	114	12	Q70467 Human bradykinin B2 r	4.39e-07
43	36	3.6	1378	17	T10666 Generic DNA sequence	1.55e-06
44	35	3.5	114	12	Q70469 Generic DNA sequence	1.55e-06
45	35	3.5	114	12	Q70465 Generic DNA sequence	1.55e-06

ALIGNMENTS

RESULT 1  
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AC Q75931;  
DT 18-AUG-1995 (first entry)  
DE Human kappa opioid receptor partial cDNA fragment.  
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;  
KW transmembrane domain; somatostatin; receptor; human; expression vector;  
KW truncate; chimaeric; assay; probe; ss.  
OS Homo sapiens.  
FH Key  
FT CDS location/Qualifiers  
FT /tag= a 102.989  
FT /product= partial human kappa opioid receptor  
FT PN W09428132-A.  
PD 08-DEC-1994.  
PR 20-MAY-1994; U05747.  
PR 20-MAY-1993; US-066296.  
PR 30-JUL-1993; US-100694.  
PR 05-NOV-1993; US-147592.  
PA (ARCH-) ARCH DEV CORP.  
PI Bell GI, Reisine T, Yasuda K;  
DR WPI; 95-022804/03.  
DR P-PSDB; R67672.  
PT Polynucleotides and peptides derived from opioid receptor  
PT polypeptides - for use in therapeutic compositions and in  
PT screening assays for useful drug substances.  
PS Claim 10; Page 236-239; 300pp; English.  
CC The partial nucleotide sequence of the novel human kappa opioid receptor  
CC gene. The gene was isolated from a human brain hippocampus cDNA library  
CC using a probe from the mouse kappa opioid receptor gene (Q75926). The  
CC gene is missing the N-terminal sequence. The C-terminal sequence is  
CC very similar to the mouse kappa opioid receptor sequence. Of the  
CC C-terminal 293 amino acids, 281 residues are identical and 6 residues  
CC have conservative substitutions. The gene encoding the human opioid  
CC receptor can be placed in a suitable expression vector for production of  
CC the protein in a cell. The opioid receptors thus produced are useful for  
CC the development of novel assays designed to select or improve substances,  
CC capable of interacting with the opioid receptor proteins, for use in  
CC diagnosis, drug design and therapeutic applications.  
SQ Sequence 1000 BP; 238 A; 253 C; 225 G; 278 T;



Query Match	99.88;	Score 992;	DB 13;	Length 1000;
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QY	601	tcaaganngtccggtcccttcttctgtctcccgagagaagaatlncaacctggtgaagatca	660
Db	661	ccagactggtctcctggtgtgtgtgagcgtctctgtctgtctgtgacctcccatccacatat	720
QY	661	ccagactggtctcctggtgtgtgtgagcgtctctgtctgtctgtgacctcccatccacatat	720
Db	721	tcatctgtgtggaagcctctggygagcaccctcccaacagcacagctgtctctctccagctatt	780
QY	721	tcatctgtgtggaagcctctggygagcaccctcccaacagcacagctgtctctctccagctatt	780
Db	781	actctgcatacgcccttaggctatataccaacagtagcctgaatcccatctctctagcctttc	840
QY	781	actctgcatacgcccttaggctatataccaacagtagcctgaatcccatctctctagcctttc	840
Db	841	ttgatgaaaacttcaagcgtgtttccggygacctgtcttccaactgaagatgagnatgg	900
QY	841	ttgatgaaaacttcaagcgtgtttccggygacctgtcttccaactgaagatgagnatgg	900
Db	901	eggcgnagagcaactagcagagtcggaatatagatccagatccctgtcttacctgagggaga	960
QY	901	agccgnagagcaactagcagagtcggaatatagatccagatccctgtcttacctgagggaga	960
Db	961	tcgatgggatgtgaataaaaccagtatgtactagtgcgtgga 1000	
QY	961	tcgatgggatgtgaataaaaccagtatgtactagtgcgtgga 1000	

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RESULT 2
ID T12550 standard; cDNA; 1142 BP.
AC T12550;
DEF 03-SEP-1996 (first entry)
DE Human kappa opioid receptor cDNA.
KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
KW neurology; diagnosis; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1142
FT /tag= a
FT /product= kappa.opioid_receptor
FT /note= "incomplete termination codon"
PN M09601898-A1.
PF 25-JAN-1996.
PD 07-JUL-1995; F00912.
PR 11-JUL-1994; FR-008531.
PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kieffer B, Simonin F;
DR WPI; 96-097628/10.
DR P-PSDB; R88722.
PT New nucleic acid encoding the human Kappa opioid receptor - useful
PT in diagnosis and therapy, and for isolating receptor ligands and
PT modulators
PS Claim 3; Page 13-15; 30pp; French.
CC This sequence codes for the human kappa opioid receptor and was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridised with a murine delta receptor cDNA
CC probe. Nucleotide probes derived from the kappa opioid receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opioid
CC receptors.
SQ Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T;

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Query Match	86.2%;	Score 857;	DB 20;	Length 1142;
Best Local Similarity	98.7%;	Pred. No. 0.00e+00;		
Matches	862;	Conservative	0;	Mismatches 11; Indels 0; Gaps 0;

D	257	gatacacaagaatgaagacagcaaccaacattacatatattaaacctggtcttggcagatg	316
Q	100	GATACACAAAGATGAAGACAGCAACCAACATTTCATATTTAACCTGGCTTTGGCAGATG	159
D	317	cttagtactacaacaacatgccccttcagagtaaggtctacttgatgnaattccgtgccct	376
Q	160	CTTAGTACTACAACCATGCCCCCTTCAGAGTAAGGCTCTACTTGATGAATTCCTGGCCTT	219
D	377	ttgggagatgctcgtgtgcaagatagtaattccattgattactacaacatgttcaaccagca	436
Q	220	TTGGGAGATGCTCTGTGCAAGATAGTAATTTCATTGATTACTACAACATGTTCAACCAGCA	279
D	437	tcttcaccttgacaacatgatagcgttggacgcgtacattgcccgtgtgccaacccgctbaag	496
Q	280	TCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGTGCCACCCCGTGAAG	339
D	497	ctttgacctccgcacaccccttgaagggcaaatcatcaatatctgcattctgctcgtgt	556
Q	340	CTTTGACCTCCGCACACCCCTTGAAGGCAAGATCATCAATACTCGCATCTGGCTGCTGT	399
D	557	cgtcatctgttggcatctctgcacaatagtccttggaggcaaccaagtcaagggaagcgtcg	616
Q	400	CGTCATCTGTTGGCATTCTTGCAATAGTCCCTTGAGGCAACCAAGTCAGGGAAGGTGTGG	459
D	617	atgtcaattgagtgtcccttcaggttccacagatgatgactaattccctgttggacctctca	676
Q	460	ATGTCAATTGAGTGTCTGCTTGCAAGTCCAGATGATGACTACTCCCTGTTGGGACCTCTTCA	519
D	677	tgaagatctgcgtcttcaattcttgcccttcgtgatccctgtctccatcatcatcgtctgct	736
Q	520	TGAAGATCTGCGCTTTCATCTTTGGCCTTCGTGATCCCTGTCCATCATCATCATCGTCTGCT	579

Db	737	aacccctgatgatacctgcgtctcaagagcgctccgctccttctctggctcccagagaagaag	796
OY	580	ACACCCTGATGATCCTGGCGTCTCAAGANNGTCCGGCTCCTTCGTGECTCCCCGAGAAGAAAG	639
Db	797	atcgaaacctgcgtagatcacccagactgctcctgtygtgytgycagtcttcgtcgtct	856
OY	640	AINNCAACCTGC GTAGGATCACAGACTGGTCTGGTGSTGGTGGSCAGTCTTCGTGCTCT	699
Db	857	gctggactccccattcacatatatcatcctctgtyggagcctctgygggaacactcccacagca	916
OY	700	GCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGGAGCACCTCCCACAGCA	759
Db	917	cagctgctctctccagctattacttctgcatacgccctlaggcgtataccaacagtagcctga	976
OY	760	CAGTGTCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTATACCAACAGTAGCCTGA	819
Db	977	atcccatctctctacgccctttcttgtatgtaaaactccaacpgtgtttccgggactctgct	1036
OY	820	ATCCCATTTCTCTACGCCCTTTCTTGATGAAGAAACTTCAAGGGGTGTTCCGGGACITTCGTCT	879
Db	1037	tcccactgaagatgaggatggagcggcgagagcacctagcagagtlccgnaatacacgttcaag	1096
OY	880	TTCACACTGAAGATGAGNATGGAGCGGCNNAGAGCACACTAGAGAGTCCGAAATACAGTTCAAG	939
Db	1097	atcctgcttaacctgagggacaatcgatgggatga 1129	
OY	940	ATCTGCTTACCCTGAGGGAGATCGATGGGATGA 972	

RESULT	3
ID	Q75926 standard; DNA; 1410 BP.
AC	Q75926;
DT	17-AUG-1995 (first entry)
DE	Mouse kappa opioid receptor MORK1 cDNA.
KW	Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW	transmembrane domain; somatostatin; receptor; human; expression vector;
KW	truncate; chimaeric; assay; probe; ss.
OS	Mus musculus.
FH	Key
FT	Location/Qualifiers
FT	CDS 186..1328
FT	/*tag= a
FT	/product= mouse kappa opioid receptor
PN	W09428132-A.
PD	08-DEC-1994.
PE	20-MAY-1994; U05747.
PR	20-MAY-1993; US-066296.
PR	30-JUL-1993; US-100694.
PR	05-NOV-1993; US-147592.
PA	(ARCH-) ARCH DEV CORP.
PI	Bell GI, Reisine T, Yasuda K;
DR	WPI; 95-022804/03.
DR	P-PSDB; R67669.
PT	Polynucleotides and peptides derived from opioid receptor
PT	polypeptides - for use in therapeutic compositions and in
PT	screening assays for useful drug substances.
PS	Claim 10; Page 207-211; 300pp; English.
CC	The nucleotide sequence of the novel mouse kappa opioid receptor gene
CC	MORK1. The gene was isolated from a mouse brain cDNA library using a
CC	fragment (amplified from the cDNA library with primers Q75929-30) as a
CC	probe. The primers are based on the conserved sequences present in the
CC	second and third transmembrane domains of somatostatin (SRIF) receptor
CC	subtypes SSTRL, SSTRL2 and SSTRL3. The 1.2 kb PstI fragment from the mouse
CC	kappa opioid receptor clone, lambda msl-1, was subcloned into the CMV
CC	promoter-based expression vector pCMV-6b. The resultant construct
CC	pCMV-msl-1 was transfected into COS-1 cells for protein production. The
CC	gene encoding the opioid receptor can be used to produce complete,
CC	truncated or chimaeric opioid receptor proteins. The opioid receptors
CC	thus produced are useful for the development of novel assays designed to
CC	select or improve substances, capable of interacting with the opioid
CC	receptor proteins, for use in diagnosis, drug design and therapeutic
CC	applications.
Q	Sequence 1410 BP; 322 A; 360 C; 337 G; 391 T;

Query Match	67.4%;	Score 670;	DB 13;	Length 1410;
Best Local Similarity	87.7%;	Pred. No. 0.00e+00;		
Matches	790;	Conservative	0;	Mismatches 108; Indels 3; Gaps 2;
Db 442	gatacacgaagatgaagaccgcaaccaacatactacatatatttaacctgttggcagatg			501
QY 100	GATACACAAGATGAAGACAGCACCAACCAATTACATATTTAACTGCTTTGGCAGATG			159
Db 502	cttggttactaacactatgcccccttcagagtgctgtctactatgaaattcttggcct			561
QY 160	CTTAGTACTACCAACCATGCCCCCTTCAGAGTAGCGGTCTACTGTGATGAATTCCTGGCCCT			219
Db 562	ttggagatgtygtatagcaagattgtcatttcocattgactactacaacatgtttaccagca			621
QY 220	TTGGGAGATGTGCTGTGCCAAGATAGTAATTTCCATTGATTACTACACATGTTCCACCAGCA			279
Db 622	tattcaaccttgacccaatgatgagtgtggaccgctacatttgtctgtgtgccacccttgaag			681
QY 280	TCTTCACCTTGACCATGATGAGCGGTGGACCGCTACATTGGCGGTGTGCCACCCCGTGAAG			339
Db 682	cttggacctccgaacacacctttgaaagcaaatcatcatcacatctgcatttggctcctg			741
QY 340	CTTTGGACTTCCGCACACCCCTTGAAGGCAAGATCATCATATCTTGCACTCTGGCTGTGT			399
Db 742	catcatctgttggatatatcagcgaatgtccttggagggcaccacaagtcaagggaagatgtg			801
QY 400	CGTCATCTGTGGCATCTCTGCCAATAGTCCCTTGAGGCGACCAAGTCAAGGGAAGGTGTG			459
Db 802	atgtcaattgaatgtctccttgcagtttccctgatgatgaatatctcctgttggagatcttca			861
QY 460	ATGTCAATTGAGTGTGCTGTGTCAGATTCCAGATGATGACTACTCTGTGTGGGACCTCTTCA			519
Db 862	tgaagatctgtgtcttcgtcttcttgccttgtgatcccaagtcctcatcatattgtctgt			921
QY 520	TGAAGATCTGGCTCTTCATCTTTGCCCTTCGTGATCCCTGTCTCATTCATCATCTGTCT			579
Db 922	acacccctgatgatcctgcgcctgaaagatgtccggtcctctgtctgctcccgagagaag			981
QY 580	ACACCCCTGATGATCTCTGCGTCTCAAGANNGTCCGGCTCCCTTCTGTGGCTCCCGAGAGAAAG			639
Db 982	accgaaatctccgcgcgcatcaccaagctggtgtgtgtagatgtgcagttctcatcatct			1041
QY 640	ATTNCAACCTGCGTAGGATCACCAAGACTGGTCTGTGTGGTGGCAGTCTTGCTGTCT			699
Db 1042	gttggaccccccatcacatctttatcctgtgtgaggtctctgggaagcaacctccacagca			1101
QY 700	GCTGGACTCCCATTCACATATTTCATCTCTGGTGGAGGCTGTGGGGAGCACCTCCACAGCA			759
Db 1102	caagtcgccctctccagctatctattctgtattgtcccttgggttatacaacagcagcctga			1161
QY 760	CAGTGTCTCTCTCCAGCAATTACTTCTGCATCGCCCTTAGGCTATACCAACAGTAGCCTGA			819
Db 1162	atcctgttctctatgctcttctgtgatgaaaacttcaagcgtgttlltagggacttctgct			1221
QY 820	ATCCCATTTCTCTACGCCCTTTCTTGATGAAGAACTTCAAGCGGTGTTCCGGGACTTCTGCT			879
Db 1222	tcocctattaagatgcgaatgagcgccagagcaaccaatagaglttagaacaacagttcagg			1281
QY 880	TTCCACTGAAGATGAGNATGGAGCGCGMAGAGCACCTAGCAGAGTCCGAAATACAGTTTCAGG			939
Db 1282	atcctgtctccatgag--agat-gtgggaaggatgaataagccagtatgactagtcgtg			1338
QY 940	ATCCTGCTTACCTTGAGGGAGATCGATGGATGATGAATTAACAGTAGTAGTAGTGTGTG			999
Db 1339	a 1339			
QY 1000	A 1000			

RESULT	4
ID	Q86725 standard; cDNA; 2481 BP.
AC	Q86725;
DT	01-DEC-1995 (first entry)





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QY 279 ATCTTACCTTGACCATGATGAGCGTGGACCGCTACATTCGCCGTGTGCCACCCCGTGAAG 338
Db 767 gccttagatttcogtactccccgaatgccaaattatcaatgtctgcaactgatactc 826
QY 339 GCTTTGGACTTCCGACACACCCCTTGAAGGCAAGATCAATATCTGCACTTGGCTGCTG 398
Db 827 tcttcagccattggtctcttcctgtaatgttcattggtctacaacaaatacagggcaagt-tc 885
QY 399 TCGTCATCTGTGGCATCTCTGCAATAGTCTTGGAGGACCAAGTCAGGGAAGGTGTC 458
Db 886 catag-attg--taaca-cttctcattccaacctgtactgg-gaaaac-ctgc 938
QY 459 GATGTCATTGAGTGTGCTTGTGACAGTTCACAGATGATGACTACTCCTGGTGGGACCTCTTC 518
Db 939 -tgaagatcgtgtttcattcttcgccttcattatgccagtgctcattacattaccgtgtgc 997
QY 519 ATGAAGATCTGGGCTCTTCATCTTGGCTTGTGATCCCTGTCTCATTCATCATCGTCTGC 578
Db 998 tatgactgatgatctctgagcctcaagaagtccgcagtctctctggtctccaaagaagaag 1057
QY 579 TACACCCCTGATGATCCTTGCCTCTCAAGANNGTCCGGCTCCTTGTGGCTCCCGAGAGAAA 638
Db 1058 gacaggaatcttcgaagagatcaccaggaatggtgtgtgtgtgtgtgtgtgtgtgtgtgtc 1117
QY 639 GATNNCAACCTGCGTAGGATCACCAAGACTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTG 698
Db 1118 tgcgtgactcccatcattcacattacgtcatttaagccttggtttacaatccagaact 1177
QY 699 TGCTGACTCCCATTCACATATTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 758
Db 1178 ac-gttccagactgttctgtgcaactctgcaattgctctaggttacacaaacagctgct 1236
QY 759 ACAGCTGCTCTCTCCAGCTATT-ACCTTGTGATCGCCTTAGGCTATACCAACAGTAGCCT 817
Db 1237 caaccacgctcttattatgcatcttcgtgatgaaacttcaaacgattgcttcagagagttctg 1296
QY 818 GAATCCCATTTCTTACGCGCTTTCTTGATGAAAACTTCAAGCGGTGTTCCGGGACTTCTG 877
Db 1297 tatccca 1303
QY 878 CTTTCCA 884
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RESULT 6
ID Q93102 standard; cDNA; 2160 BP.
AC Q93102;
DT 11-DEC-1995 (first entry)
DE Human mu opiate receptor cDNA.
KW Mu Opiate receptor; hMOR; opiate agonist; opiate antagonist;
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 213..1415
FT /*tag= a
PN WO9520667-A1.
PD 03-AUG-1995.
PR 30-JAN-1995; U01144.
PR 28-JAN-1994; US-188275.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH ) US SEC DEPT HEALTH.
PI Johnson PS, Persico AM, Uhl G, Wang J;
DR WPI; 95-275452/36.
DR P-PSDB; R76780.
PT New DNA encoding human mu opiate receptor - used esp. for screening
PT cpds. for activity as opiate agonists or antagonists
PS Claim 4; Page 24-25; 49pp; English.
CC hMOR cDNA was obtd. from a human cerebral cortical cDNA library
CC screened with fragments of a rat mu opiate receptor. Cloned hMOR
CC DNA can be used as probes to examine the structure and function of
CC hMOR genes or to screen individuals for susceptibility to drug
CC abuse. Expression in e.g. COS cells allows production of
CC recombinant hMOR1.
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SQ Sequence 2160 BP; 563 A; 566 C; 455 G; 576 T;
Query Match 28.4%; Score 282; DB 15; Length 2160;
Best Local Similarity 71.2%; Pred. No. 2.66e-171;
Matches 560; Conservative 0; Mismatches 216; Indels 11; Gaps 10;
Db 501 agatacaccagaatgaagactgccaccacatctacatttcaacctgtctgagagat 560
QY 99 AGATACACAAGATGAAGACAGCAACCAACATTATCATATTTAACTGGCTTGGCAGAT 158
Db 561 gccttagccaccagtaacctggcccttcagagagtgtgaattaccataatggaacatgcca 620
QY 159 GCTTTAGTTACTACAACCATGCGCTTTCAGAGTACGCTACTTCAATGAATTCCTGGCCT 218
Db 621 ttggaacacatcctltgcaagatagtgatctcatagattactataacatgttccaccagc 680
QY 219 TTTGGGAGTGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACACATGTTCAACGAC 278
Db 681 atataccctctgcaccatgagtgttgatcgatacatctgcagctctgccacctgtcaag 740
QY 279 ATCTTCAACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGTGCCACCCCGTGAAG 338
Db 741 gccttagatttcogtactccccgaatgccaaattatcaatgtctgcaactgatactc 800
QY 339 GCTTTGACCTTCCGACACACCCCTTGAAGGCAAGATCATCAATCTGCATCTGGCTGCTG 398
Db 801 tcttcagccattggtctctcctgtaatgttcatgtgctacaacaaatacaggaaggt-tc 859
QY 399 TCCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCAACCAAGTCAAGGAGAGGTGTC 458
Db 860 catag-attg--taaca-cttctcattccaacctgtactgg-gaaaac-ct-c 911
QY 459 GATGTCATTGAGTGTGCTGTGCACTTCCAGATGATGACTACTCCTGTGTGGGACTCTTTC 518
Db 912 gtgaagatcgtgttttcaatcttcgccttcattatgcaagtgctcatcattaccgtgtgc 971
QY 519 ATGAAGATCTGCGTCTTCACTTGTGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 578
Db 972 tatgactgatgatcttgcgcctcaagaagtgtccgcatgctctgtgctccaaagaagaag 1031
QY 579 TACACCCCTGATGATCCTGCGCTCTCAAGANNGTCCGGCTCCTTGTGTGCTCCGAGAGAAA 638
Db 1032 gacaggaatcttcgaagagatcaccaggaatggtgtgtgtgtgtgtgtgtgtgtgtgtgtc 1091
QY 639 GATNNCAACCTGCGTAGGATCACCAAGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 698
Db 1092 tgcgtgactcccatcattacattacgtcattcaaaagccttggttacatccagaact 1151
QY 699 TGCTGACTCCCATTCACATATTCATCTCTGTGTGAGGCTCTGGGAGACACCTCCACAGC 758
Db 1152 ac-gttccagactgttctgtgcaactctgcaattgctctaggttacacaaacagctgct 1210
QY 759 ACAGCTGCTCTCTCCAGCTATT-ACCTTGTGATCGCCTTAGGCTATACCAACAGTAGCCT 817
Db 1211 caaccacgctcttattatgcatcttcgtgatgaaacttcaaacgattgcttcagagagttctg 1270
QY 818 GAATCCCATTTCTTACGCGCTTCTTGATGAATAAATTCAAGCGGTGTTCCGGGACTTCTG 877
Db 1271 tatccca 1277
QY 878 CTTTCCA 884
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RESULT 7
ID Q79199 standard; cDNA; 2070 BP.
AC Q79199;
DT 19-APR-1995 (first entry)
DE Rat mu-subtype opioid receptor cDNA.
KW Mu-subtype opioid receptor; mSOR; drug addiction; ds.
OS Rattus rattus.
FH Key Location/Qualifiers
FT CDS 83..1154
FT /*tag= a
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/product= Mu-subtype\_opioid\_receptor  
FT BP-612345-A.  
PN 31-AUG-1994.  
PD 09-FEB-1994; 101968.  
PF 26-FEB-1993; US-026140.  
PR (AMCY ) AMERICAN CYANAMID CO.  
PI Corbett MJ, Eppler CM, Shieh H, Zysk JR;  
DR WPI: 94-265963/33.  
P-PSDB; R65188.  
DR pure mu-type opioid receptor protein - and nucleic acid coding  
PT for it  
PS Claim 1; Fig 11; 39pp; English.  
CC R65188 is the rat mu-subtype opioid receptor protein purified  
CC from rat brain membranes, with biotinyl-b-endorphin (R56666)  
CC as its ligand. It is encoded by the nucleotide sequence Q79199  
CC which was synthesised using Q71022 and Q71023 as PCR primers.  
CC R65188 is useful for identifying other receptor subtypes, for  
CC screening new opioid ligands, and for studying mechanisms of  
CC opioid action, e.g. drug addiction.  
SQ Sequence 2070 BP; 526 A; 564 C; 423 G; 557 T;

Query Match 28.1%; Score 279; DB 12; Length 2070;  
Best Local Similarity 70.4%; Pred. No. 3.27e-169;  
Matches 553; Conservative 0; Mismatches 224; Indels 9; Gaps 7;

Db 248 agatacaccaaaatgaagactgccaccaacatctacatttcaacctgtctcagagac 307  
QY 99 AGATACACAAGATGAAGACAGCAACCAATTACATATTAACTGGCTTTGGCAGAT 158  
Db 308 gccctagcagccagctacactgcccttcagagtgtcaactacctgattggagacatggccc 367  
QY 159 GCTTTAGTTACTACAACCATGCCCTTTCAAGATACGGTCTACTTGTGTAATTCTCGGCT 218  
Db 368 ttcggaacatcctctgcaagatcgatctcaatagattactacaacatgttcaccagc 427  
QY 219 TTGGGGAGTGTGCTGTGCAAGATAGTAATTCCATTGATTACTACAACATGTTCAACGAGC 278  
Db 428 atattcacccctctgcaccatgagcgtygaccgctacattgtctcgcaccacgtcaaa 487  
QY 279 ATCTTCACCTTGAACCATGATGAGCGGTGAGCCGTACATTTGCCGTGTGCCACCCCGTGAAG 338  
Db 488 gccctgagatttcggtaccccccgaaatgccaaaatcgtcaacgctctgcaactgatacctc 547  
QY 339 GCTTTGGACTCCGCACACACCCTTGAAGGCAAGATCATCAATATCTGCATCTGGCTGCTG 398  
Db 548 tcttctgcatcgtctgcaagatcgatctcaatagattactacaacatgttcaccagc 606  
QY 399 TCGTCATCTGTGGCATCTCTGCAATAGTCTTGGAGGCAACCAAGTCAAGGGAAGGTGTC 458  
Db 607 catag-attgcaacct-cacgttct-cccccccaac--ctggtactgggagaacctgctc 661  
QY 459 GATGTCAATTGAGTGTGCTTGGCAGTTCCCGAGATGACTACTCCTGTGGGAGACCTCTTC 518  
Db 662 a--aa-atctgtgtcttatacttcgcttcaatcgccggtccatcatcaactgtgtgt 718  
QY 519 ATGAAGATCTGGCTCTTCATCTTGGCTTCGATCCCTGTCTCATCATCATCTGCTGTC 578  
Db 719 taagcgctgatatcttaagactcaagagcgcttcgcatgtctatcgggctccaaagaag 778  
QY 579 TACACCCCTGATGATCTGCGTCTCAAGANNNGTCGCTCTTCTGTGCTCCCGAGAGAAA 638  
Db 779 gaacaggaatctgcgagagatcacccggatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 838  
QY 639 GATTNCAACCTGGCTAGGATCACCAAGACTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 698  
Db 839 tgctggaaccccatcacatctacgtcatcatcaagcgctgatacagattccaagaaacc 898  
QY 699 TGCTGAGCTCCCATTCACATATTCATCTGCTGTGAGGCTCTGGGGAGCACCTCCACAGC 758  
Db 899 acatttcagaccgttctcctggcaactctcgtcatgtcttgggttacacgaacagctgctg 958  
QY 759 ACAGCTGCTCTCTCCAGCTAATTAATCTCTGCATCGCCTTAGGCTATACCAACAGTAGCCTG 818

Db 959 aatccagttctttaaagccttctcgtgatgaaacttcaagcgatgcttcagagagttctgc 1018  
QY 819 AATCCATTCTCTACGCCCTTTCTTGATGAAGAACTTCAAGCGGTGTCTCCGGACTTCTGC 878  
Db 1019 atoccca 1024  
QY 879 TTTCCA 884

RESULT 8  
ID Q89222 standard; cDNA; 1618 BP.  
AC Q89222; 20-OCT-1995 (first entry).  
DE Rat mu opioid receptor cDNA.  
KW Mu opioid receptor; MOR-1; gene therapy; diagnostic; ss.  
OS Rattus sp.  
FH Key Location/Qualifiers  
FT CDS 214..1410  
FT CD5  
PN W09507983-A.  
PD 23-MAR-1995.  
PE 13-SEP-1994; U10358.  
PR 13-SEP-1993; US-120601.  
PA (INDV ) UNIV INDIANA FOUND.  
PI Yu L;  
DR WPI: 95-131351/17.  
DR P-PSDB; R71964.  
PT New nucleic acid encoding new human mu opioid receptor - and  
PT related vectors, transformed cells, antibodies etc., useful in  
PT diagnosis, treatment and drug screening.  
PS Disclosure; Page 190-194; 266pp; English.  
CC A 365 bp fragment of the mouse delta opioid receptor was used to  
CC screen a rat brain cDNA library under low stringency conditions.  
CC One positive clone included the sequence given in Q89222, encoding a  
CC mu opioid receptor, MOR-1 (R71964). MOR-1 was stably expressed in  
CC transfected CHO cells.  
SQ Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T;

Query Match 27.9%; Score 277; DB 14; Length 1618;  
Best Local Similarity 70.2%; Pred. No. 8.09e-168;  
Matches 552; Conservative 0; Mismatches 225; Indels 9; Gaps 7;

Db 496 agatacaccaaaatgaagactgccaccaacatctacatttcaacctgtctcagagac 555  
QY 99 AGATACACAAGATGAAGACAGCAACCAATTACATATTAACTGGCTTTGGCAGAT 158  
Db 556 gccctagcagccagctacactgcccttcagagtgtcaactacctgattggagacatggccc 615  
QY 159 GCTTTAGTTACTACAACCATGCCCCCTTTCAGAGTACGGTCTACTTGAATTCCTGGCCT 218  
Db 616 ttcggaacatcctctgcaagatcgatctcaatagattactacaacatgttcaccagc 675  
QY 219 TTGGGGAGTGTGCTGTGCAAGATAGTAATTTCATTGATTACTACAACATGTTCAACGAGC 278  
Db 676 atattcacccctctgcaccatgagcgtygaccgctacattgtctgtgccaccagtcacaa 735  
QY 279 ATCTTCACCTTGAACCATGATGAGCGGTGACCGCTTACATTGGCCGTGTGCCACCCGTAAG 338  
Db 736 gccctgagatttcgtaaccccccgaaatgccaaaatcgtcaacgctcgaactgatacctc 795  
QY 339 GCTTTGAGCTTCCGCACACCCCTTGAAGGCAAGATCATCAATATCTGTGCTGCTG 398  
Db 796 tcttctgcatcgtctgtcgtgtatgttcaatgttcagtgcaacacaaatagagcagggtgtc 854  
QY 399 TCGTCATCTGTGGCATCTCTGCAATAGTCTCTTGAAGGCAACCAAGTCAAGGGAAGGTGTC 458  
Db 855 catag-attgcaacct-cacgttct-cccccccaac--ctggtactgggagaacctgctc 909  
QY 459 GATGTCAATTGAGTGTGCTTGCAGTTCGCCAGATGATGACTACTCCTGTGTGGGACCTCTTC 518  
Db 910 a--aa-atctgtgtcttatacttcgcttcatcatgcccagatcctcatcatcaactgtgtgt 966  
QY 519 ATGAAGATCTGGCTCTTCATCTTGGCTTGTGTGATCCCTGTCTCATCATCATCTGCTGTC 578

Db 967 tacggcctgatgatcttaagactcaagagcgttcgcattatcgggctcccaagaaaag 1026  
||| ||||| ||| ||| ||||| ||| ||| ||||| ||| |||  
QY 579 TACACCCCTGATGATCCCTGGCTCTCAAGANNGTCCGGCTCCTTCTGGCTCCCGAGAGAAA 638  
Db 1027 gacaggaatctgcgcagagatcaaccgcatgtgtcgtgtgtcgtgtattatcgtc 1086  
||| ||| ||||| ||||| ||| ||| ||||| ||| ||| |||||  
QY 639 GATNNCAACCTGCGTAGAGATCAACGAGACTGGTCCGTGGTGGTGCGAGCTTCGTCGTC 698  
Db 1087 tgcctgaccccccatccacatctacgtcatcatcaaaagcgtgatcaacgattccagaacc 1146  
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QY 699 TGCTGGACTCCCATTCACATATTTCATCCTGGTGAAGGCTCTGGGAGCACCTCCACAGC 758  
Db 1147 acattcagaccggttcctcgtgcactctcgtcattgtgttggttacacgaaagctgcctg 1206  
||| | ||| ||||| ||| ||||| ||| ||| ||| ||||| |||||  
QY 759 ACAGCTGCTCTCTCCAGCTATTACTTCTGCACTCGCCTTAGGCTATACCAACAGTAGCCTG 818  
Db 1207 aatccagttctttaagccttcctcgtgatgataaaactcaagcgatgcttcagagaagttctgc 1266  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 819 AATCCCATTTCTCTACGCCCTTCTTGATGAAGAACTTCAAGCGGTGTTCCGGGACTTCTGC 878  
Db 1267 atccca 1272  
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QY 879 TTTCOA 884

RESULT 9  
ID Q89223 standard; cDNA; 1618 BP.  
AC Q89223;  
DT 20-OCT-1995 (first entry)  
DE Transcription regulatory protein cDNA.  
KW Mu opioid receptor; MOR-1; gene therapy; diagnostic;  
KW Ratius sp.  
OS Ratius sp.  
FH Key Location/Qualifiers  
FT CDS 339..1235  
FT /\*tag= a  
PN WO9507983-A.  
PD 23-MAR-1995.  
PE 13-SEP-1994; U10358.  
PR 13-SEP-1993; US-120601.  
PA (INDV ) UNIV INDIANA FOUND.  
PI Yu L;  
PI WPI; 95-131351/17.  
DR P-PSDB; R71965.  
PT New nucleic acid encoding new human mu opioid receptor - and  
PT related vectors, transformed cells, antibodies etc., useful in  
PT diagnosis, treatment and drug screening.  
PS Disclosure; Page 199-203; 266pp; English.  
CC A 365 bp fragment of the mouse delta opioid receptor was used to  
CC screen a rat brain cDNA library under low stringency conditions.  
CC One positive clone included the sequence given in Q89222, encoding a  
CC mu opioid receptor, MOR-1 (R71964). Sequence analysis revealed a  
CC alternative reading frame (Q89223) encoding a zinc  
CC finger-containing transcription regulatory protein (R71965).  
SQ Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T;

Query Match 27.9%; Score 277; DB 14; Length 1618;  
Best Local Similarity 70.2%; Pred. No. 8.09e-168;  
Matches 552; Conservative 0; Mismatches 225; Indels 9; Gaps 7;

Db 496 agatacaccaaatgaagactgccaacaacatctacatttcaacctgtctgtgcagac 555  
||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||  
QY 99 AGATACACAAAGATGAAGAGAGCAACCAACATTACATTTTAACTGGCTTGGCAGAT 158  
Db 556 gccctagcagcagctacacgtcccttccagagtggtcaactacctgatggaacatggccc 615  
||| ||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 159 GCTTAGTACTACAAACCAACGCCCCCTTCAGAGTAGCGTCTACTTGATGAATTCTGCGCT 218  
Db 616 ttcggaaccatcctctgcaagatcgtgatctcaatagattactacaacatgttaccagc 675  
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QY 219 TTTGGGATGTGCTGTGCAAGATAGTAATTTCATTGATTACTACAAACATGTTACACGAC 278

Db 676 atattcaacctctgcacccaatgagcgtgagccgtacatltgctgtctgccaccagttcaa 735  
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QY 279 ATCTTCACCTTGACCATGATGAGCGTGGACCGGCTACATTTGCCGTGTGCCACCCCGTGAAG 338  
Db 736 gccctgatttcggtacccccgaatatgccaaaatcgtcaacgctcgaactgatatcctc 795  
||| ||| ||||| ||||| ||| ||| ||||| ||| ||| ||||| |||||  
QY 339 GCTTTGACTTCCGACACACCCCTTGAAGGCAAGATCATATATCTGCACTTGCGTGTG 398  
Db 796 tcttctgccatcggtctgtcctgtaatgttcatggtgcaaacacaataacagggcagg-gtc 854  
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QY 399 TGCTCATCTGTGGCATCTCTGCAATAGTCTTGGAGGCACCAAGTCAAGGAAAGGTGTC 458  
Db 855 catag-atgcaacct-caagttct-cccacccaac--ctggtactgggagaacctgtc 909  
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QY 459 GATGTCATTGAGTGTGCTGCTTGACGTTCCAGATGATGACTACTCCTGGTGGGACCTCTTC 518  
Db 910 a--aa-atcgtgtcttattcttcgttcacatcgcgatccctcatcatcactgtgtgt 966  
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 519 ATGAAGATCTGGGCTCTTCATCTTGCCCTTGATGCCCTGTCCCTCATCATCGTCTGC 578  
Db 967 tacggcctgatgatcttaagactcaagagcgttcgcattatcggtatcggtccaaagaaag 1026  
||| ||||| ||||| ||| ||||| ||| ||| ||| ||||| |||||  
QY 579 TACACCCCTGATGATCCCTGGCTCTCAAGANNGTCCGGCTCCTTCTGGCTCCCGAGAGAAA 638  
Db 1027 gacaggaatctgcgcagagatcaaccgcatgtgtgtgtgtgtgtatattatcgtc 1086  
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 639 GATNNCAACCTGCGTAGAGATCAACGAGACTGCTCTGTGGTGGTGCAGTCTTCGTCGTC 698  
Db 1087 tgcctgaccccccatccacatctacgtcatcatcaaaagcgtgatcaacgattccagaacc 1146  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 699 TGCTGGACTCCCATTCACATATTTCATCCTGGTGAAGGCTCTGGGAGCACCTCCACAGC 758  
Db 1147 acattcagaccggttcctcgtgcactctcgtcattgtgttggttacacgaaagctgcctg 1206  
||| | ||| ||||| ||| ||||| ||| ||| ||| ||||| |||||  
QY 759 ACAGCTGCTCTCTCCAGCTATTACTTCTGCACTCGCCTTAGGCTATACCAACAGTAGCCTG 818  
Db 1207 aatccagttctttaagccttcctcgtgatgataaaactcaagcgatgcttcagagaagttctgc 1266  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 819 AATCCCATTTCTCTACGCCCTTCTTGATGAAGAACTTCAAGCGGTGTTCCGGGACTTCTGC 878  
Db 1267 atccca 1272  
| |||  
QY 879 TTTCOA 884

RESULT 10  
ID Q56700 standard; cDNA; 1821 BP.  
AC Q56700;  
DT 15-SEP-1994 (first entry)  
DE Sequence of murine delta opioid receptor in the DOR-1 cDNA clone.  
KW Opioid receptor; morphine; opiate; ss.  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT CDS 29..1139  
FT /\*tag= a  
PN WO9404552-A.  
PD 03-MAR-1994.  
PE 13-AUG-1993; U07665.  
PR 13-AUG-1992; US-929200.  
PA (REGC ) UNIV CALIFORNIA.  
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;  
DR WPI; 94-083099/10.  
PT P-PSDB; R48629.  
PT DNA encoding opioid receptors and antibodies against this  
PT receptor - used to express and locate these receptors, and screen  
PT cpds. for opioid (ant)agonist activity  
PS Claim 1; Fig 5; 74pp; English.  
CC A cDNA library was constructed using mRNA isolated from the NG109-15  
CC cell line. A single clone, named the DOR-1 clone was isolated.  
CC Comparisons with known sequences in GenBank showed highest homology  
CC between DOR-1 and the G-protein-coupled somatostatin receptor. Other  
CC features of the DOR-1 clone AA sequence deduced from the cDNA  
CC sequence include 3 consensus glycosylation sites at residues 18 and





DY		879 TTTCOA	884	
Dd	1309 atccca	1314		
ID	Q75927 standard; DNA;	2272 BP.		
AC	Q75927;			
DT	Mouse delta opiod receptor MOR1 cDNA.			
KW	transmembrane domain; somatostatin; receptor; human; expression vector;			
KV	truncate; chimaeric assay; probe; ss.			
OS	Mus musculus.			
FH	Key	Location/Qualifiers		
FT	CDS	12..1130		
FT	/tag= a			
PN	/product= mouse delta opiod receptor			
PD	WO9428132-A.			
DE	08-DEC-1994.			
PR	20-MAY-1994; U05747.			
PR	20-MAY-1993; US-066296.			
PR	30-JUL-1993; US-100694.			
PA	05-NOV-1993; US-147592.			
PI	(ARCH-) ARCH DEV CORP.			
DR	Bell GI, Reisine T, Yasuda K;			
PT	WPJ; 95-022804/03.			
PS	p-PESDB; R67670.			
CC	The nucleotide sequence of the novel mouse delta opiod receptor gene			
CC	mORDL. The gene was isolated from a mouse brain CDNA library using a			
CC	fragment (amplified from the CDNA library with primers Q75929-30) as a			
CC	probe. The primers are based on the conserved sequences present in the			
CC	second and third transmembrane domains of somatostatin (SRIF) receptor			
CC	subtypes SSTR1, SSTR2 and SSTR3. The 1.3 kb EcorI-SacI fragment from the			
CC	CMV promoter-based expression vector PCMV-6c. The resultant construct			
CC	pcmv-msl-2 was transfected into COS-1 cells for protein production. The			
CC	gene encoding the opiod receptor can be used to produce complete,			
CC	truncated or chimeraic opiod receptor proteins. The opiod receptors			
CC	thus produced are useful for the development of novel assays designed to			
CC	select or improve substances, capable of interacting with the opiod			
CC	receptor proteins, for use in diagnosis, drug design and therapeutic			
CC	applications.			
SQ	Sequence	2272 BP;	485 A;	665 C;
				650 G;
				472 T;
Query Match	Best Local Similarity	26.7%; Score 265;	DB 13;	Length 2272;
Matches	550; Conservative	0; Mismatches 217;	Indels 12;	Gaps 10;
Dy	240 taaccaaatgaagaccgcacaacatatcatcttcaattgtgacttgataaacgatggcg	299		
Dy	102 TACAACAAGATGAAGACGCAACCATAATTACACTTGCTTGGCAGATGCT	161		
Dy	300 ctgccacacaggcacgctgccttcacagagcgccaagtacttgtatgaaacyggcgltt	359		
Oy	162 TTAGTTACTACAACCATGCCCTTTCAGAGTAACCGGTCTACTTGAATGCCTTGGCTTT	221		
Dy	360 ggcgagctgtgtgcaaagctgtgtctttcataattgacctactacaacatgttctaagc	419		
Oy	222 GGGATGTGCTGTGCAAGATAGAATTTCATTGATTACTACAACATGTTCAACAGCATC	281		
Dy	420 ttcaaccttaacatgatgatgagcgtgacacgttacattgtgtctgcccactcgtcaagcc	479		
Oy	282 TTCACCTTGACCATGATGAGCGTIGAACCGCTACATTGCCCCGTGTGCCAACCCTGAAAGCT	341		
Dy	480 ctggaactcccgacacacagccaagccccagaagcttatcatatatgatgcattgtgggtc	539		

Query	Similarity	Score	DB	Length
342	70.5%	248	DB 11	2216
540	70.5%	248	DB 11	2216
402	70.5%	248	DB 11	2216
600	70.5%	248	DB 11	2216
462	70.5%	248	DB 11	2216
651	70.5%	248	DB 11	2216
522	70.5%	248	DB 11	2216
711	70.5%	248	DB 11	2216
582	70.5%	248	DB 11	2216
771	70.5%	248	DB 11	2216
642	70.5%	248	DB 11	2216
831	70.5%	248	DB 11	2216
702	70.5%	248	DB 11	2216
891	70.5%	248	DB 11	2216
761	70.5%	248	DB 11	2216
951	70.5%	248	DB 11	2216
819	70.5%	248	DB 11	2216



RESULT 15  
ID Q56702 standard; DNA; 2447 BP.  
AC Q56702;  
DI 15-SEP-1994 (first entry)  
DE Partial sequence of the human kappa opioid receptor  
DE genomic clone H14 (KORa).  
KW Opioid receptor; morphine; opiate; ss.  
OS Homo sapiens.  
PN W03404552-A.  
PD 03-MAR-1994.  
PF 13-AUG-1993; U07665.  
PR 13-AUG-1992; US-929200.  
PA (REGC ) UNIV CALIFORNIA.  
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;  
DR WPI; 94-083099/10.  
PT DNA encoding opioid receptors and antibodies against this  
PT receptor - used to express and locate these receptors, and screen  
PT opds. for opioid (ant)agonist activity  
PS Example; Fig 8b; 74pp; English.  
CC To isolate opiate receptor genomic clones, 300,000 human genomic  
CC clones and a similar number of mouse genomic clones were probed  
CC with the 1.1 kb mouse delta opioid receptor clone DOR-1 Pst/XbaI  
CC fragment. One mouse clone and three human genomic clones were  
CC isolated. The 3 human clones had very different EcoRI patterns  
CC which indicated that three different genes were represented by the  
CC human genomic clones which were designated H3, H14 and H20. H14 maps  
CC to chromosome 8. It encodes the human kappa opioid receptor.  
SQ Sequence 2447 BP; 683 A; 512 C; 498 G; 747 T;

Query Match 24.6%; Score 245; DB 10; Length 2447;  
Best Local Similarity 100.0%; Pred. No. 1.40e-145;  
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 cctggcctttggggatgtgtgtgcaagatagtaattccattgattactacaatgt 60  
QY 211 CCTGGCCTTTGGGGATGTGCTGTGCAAGATAGTAATTCCATTGATTACTACACATGT 270  
Db 61 tcaccagcatcttcaccttgaccatgatgagcgtgacgcgtacattgcccgtgtgccacc 120  
QY 271 TCACCAAGCATCTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCCGTGTGCCACC 330  
Db 121 ccgtgaaggccttggactccgcacacccttgaaggcaagatcacaatatctgtcatct 180  
QY 331 CCGTGAAGGCTTTGGACTTCGCAACACCCCTTGAAGGCAAGAATCAATATCTGCATCT 390  
Db 181 ggtcgtgtcgtcatctgtttgcaatctctgcaatagtcccttgaggcaccacaagtcaagg 240  
QY 391 GGCTGCTGTGTCATCTGTGGCATCTCTGCATATAGTCCCTTGAGGGCAACCAAGTCAGGG 450  
Db 241 aaggt 245  
QY 451 AAGGT 455

Search completed: Tue Aug 26 10:58:14 1997  
Job time : 162 secs.



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SUMMARY #length 380 #molecular-weight 42652 #checksum 9937

Query Match 95.8%; Score 2136; DB 14; Length 380;  
Best Local Similarity 92.9%; Pred. No. 0.00e+00;  
Matches 274; Conservative 13; Mismatches 7; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladalvttmpfgsavylmnswpfgdv1ckivisidyymfts1 146  
QY 1 YTKMKTATNIYIFNLALADALVTTMPFGSTVYLMNSWPFQDVLCIKIVISIDYNNMFTSI 60

Db 147 ftltmmsvdrylavchpvpkaldfrtprlkakiniiciwllassvgisaivlggtkvredvd 206  
QY 61 FTLTMMSVDRYIAVCHPVKALDFRTPRLKAKIINICIWLLSSVGSISAIVLGGTKVREDVD 120

Db 207 viecslqfpddegyswdlfnkicvfvfafvfpvllivcytlmlrlksvrlsgsrek 266  
QY 121 VIECCLQFPDDDYSWWDLFMKICVFIFAFAVFPVLIIVCYTLMRLKXVRLSGSREKD 180

Db 267 nrlrrltklvllvvavfiicwtpihifilvealgstshstaalsyyficialgynssln 326  
QY 181 XNLRIRITRLVLLVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFICIALGYTNSSLN 240

Db 327 pvllyafidenfkrcfrdfcfpikmmerqstnrvrntvygdpsamrdvgm-nkpv 380  
QY 241 PLYAFIDENFKRCFRDFCFPIKMMERXSTSRVNTVQDPAYLREIDGMNKPV 295

RESULT 5

ENTRY S36143 #type complete  
TITLE kappa opioid receptor - rat  
ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 10-Dec-1993 #sequence\_revision 19-Oct-1995 #text\_change 06-Sep-1996

ACCESSIONS S36143; S38825; S36102; S39015; A48789

REFERENCE S36143  
#authors Nishi, M.; Takeshima, H.; Fukuda, K.; Kato, S.; Mori, K.  
#journal FEBS Lett. (1993) 330:77-80  
#title cDNA cloning and pharmacological characterization of an opioid receptor with high affinities for kappa-subtype-selective ligands.

#accession S36143  
#status Preliminary  
#molecule\_type mRNA  
#residues 1-380 #label NIS

REFERENCE S38825  
#authors Chen, Y.; Westek, A.; Liu, J.; Yu, L.  
#journal Biochem. J. (1993) 295:625-628  
#title Molecular cloning of a rat kappa opioid receptor reveals sequence similarities to the mu and delta opioid receptors.

#accession S38825  
#status Preliminary  
#molecule\_type mRNA  
#residues 1-380 #label CHE

REFERENCE S36102  
#cross-references GB:U22001

REFERENCE S36102  
#authors Minami, M.; Toya, T.; Katao, Y.; Maekawa, K.; Nakamura, S.; Onogi, T.; Kaneko, S.; Satoh, M.  
#journal FEBS Lett. (1993) 329:291-295  
#title Cloning and expression of a cDNA for the rat kappa-opioid receptor.

#accession S36102  
#molecule\_type mRNA  
#residues 1-41, 'L', 43-380 #label MIN

REFERENCE S39015  
#authors Li, S.; Zhu, J.; Chen, C.; Chen, Y.W.; Dieriel, J.K.; Ashby, B.; Liu-Chen, L.Y.  
#journal Biochem. J. (1993) 295:629-633  
#title Molecular cloning and expression of a rat kappa opioid receptor.

#accession S39015  
#molecule\_type mRNA  
#residues 1-344, 'Y', 346-380 #label LIS

REFERENCE A48789

#authors Meng, F.; Xie, G.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9954-9958  
#title Cloning and pharmacological characterization of a rat kappa opioid receptor.  
#cross-references MUID:94052210

#accession A48789  
#status Preliminary; translated from GB/EMBL/DBJ  
#molecule\_type mRNA  
#residues 1-380 #label RES

SUMMARY #cross-references EMBL:U00442; NID:g403486; CDS\_PID:g403487  
#length 380 #molecular-weight 42688 #checksum 9972

Query Match 95.6%; Score 2132; DB 14; Length 380;  
Best Local Similarity 92.5%; Pred. No. 0.00e+00;  
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladalvttmpfgsavylmnswpfgdv1ckivisidyymfts1 146  
QY 1 YTKMKTATNIYIFNLALADALVTTMPFGSTVYLMNSWPFQDVLCIKIVISIDYNNMFTSI 60

Db 147 ftltmmsvdrylavchpvpkaldfrtprlkakiniiciwllassvgisaivlggtkvredvd 206  
QY 61 FTLTMMSVDRYIAVCHPVKALDFRTPRLKAKIINICIWLLSSVGSISAIVLGGTKVREDVD 120

Db 207 viecslqfpddegyswdlfnkicvfvfafvfpvllivcytlmlrlksvrlsgsrek 266  
QY 121 VIECCLQFPDDDYSWWDLFMKICVFIFAFAVFPVLIIVCYTLMRLKXVRLSGSREKD 180

Db 267 nrlrrltklvllvvavfiicwtpihifilvealgstshstaalsyyficialgynssln 326  
QY 181 XNLRIRITRLVLLVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFICIALGYTNSSLN 240

Db 327 pvllyafidenfkrcfrdfcfpikmmerqstnrvrntvygdpsamrdvgm-nkpv 380  
QY 241 PLYAFIDENFKRCFRDFCFPIKMMERXSTSRVNTVQDPAYLREIDGMNKPV 295

RESULT 6

ENTRY JC2434 #type complete  
TITLE kappa-opioid receptor - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 21-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 05-Apr-1995

ACCESSIONS JC2434  
REFERENCE JC2434  
#authors Nishi, M.; Takeshima, H.; Mori, M.; Nakagawara, K.; Takeuchi, T.  
#journal Biochem. Biophys. Res. Commun. (1994) 205:1353-1357  
#title Structure and chromosomal mapping of genes for the mouse kappa-opioid receptor and an opioid receptor homologue (MOR-C).

#accession JC2434  
#status  
#molecule\_type mRNA  
#residues 1-380 #label NIS

GENETICS #map\_position 1A2-3  
#introns 86/2; 204/1  
KEYWORDS receptor  
SUMMARY #length 380 #molecular-weight 42630 #checksum 9705

Query Match 94.8%; Score 2114; DB 14; Length 380;  
Best Local Similarity 92.5%; Pred. No. 0.00e+00;  
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladalvttmpfgsavylmnswpfgdv1ckivisidyymfts1 146  
QY 1 YTKMKTATNIYIFNLALADALVTTMPFGSTVYLMNSWPFQDVLCIKIVISIDYNNMFTSI 60

Db 147 ftltmmsvdrylavchpvpkaldfrtprlkakiniiciwllassvgisaivlggtkvredvd 206  
QY 61 FTLTMMSVDRYIAVCHPVKALDFRTPRLKAKIINICIWLLSSVGSISAIVLGGTKVREDVD 120

[illegible]

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QY      61 FTLTMSVDRIYAVCHPVKALDEFTPLKAKIINICIMWLLSSSVGISAIVLGTTKVEDVD 120
Db      215 -idctltfshptw-ywenlklcwfifafimpvllitvcyglmrlrksvrmlsgsked 272
          ||| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      121 VIECCLQFPDDYSWWDLFMKICVFIFAIVIPVLIITVCYTLMILRLKXVRLLSGSREKD 180
Db      273 nlriritmrvlvavfvicwcpbhivylkalittipettftqtswhfciaiytnscln 332
          ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      181 XNLRIRTRLVVVAAVFVWCWPTPIHIFLIVEALGSTSHSTAALSSYYFCIALGTNSSLN 240
Db      333 pvlvafldenfkrcfrceiptstieqnsarirqrutrehpstantvd 381
          |:||||| : : : : : : : : : : : : : : : : : : : : : : : :
QY      241 PILYAFLDENFKRCFRDFCEPLKMXMERXSTSRVF-NTVQDPAYLLREID 288

RESULT      8
ENTRY        S34593 #type complete
TITLE        mu opiate receptor - rat
ORGANISM     #formal_name Rattus norvegicus #common_name Norway rat
DATE         10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change
              06-Sep-1996
ACCESSIONS   S34593; A48799; I58154
REFERENCE    S34592
#authors     Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.
#journal     FEBS Lett. (1993) 327:311-314
#title       Primary structures and expression from cDNAs of rat opioid
              receptor delta- and mu-subtypes.
#accession   S34593
              ##molecule_type mRNA
              ##residues 1-398 ##label FUK
REFERENCE    A48799
#authors     Wang, J.
#journal     Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10230-10234
#title       Mu opiate receptor: cDNA cloning and expression.
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#authors     Thompson, R.C.; Mansour, A.; Akil, H.; Watson, S.J.
#journal     Neuron (1993) 11:903-913
#title       Cloning and pharmacological characterization of a rat mu
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#cross-references MUID:94059560
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Db      215 -idctltfshptw-ywenlklcwfifafimpvllitvcyglmrlrksvrmlsgsked 272
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QY      121 VIECCLQFPDDYSWWDLFMKICVFIFAIVIPVLIITVCYTLMILRLKXVRLLSGSREKD 180
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          06-Sep-1996
ACCESSIONS      I56553; A38991; S41075; S51215
REFERENCE      I56553
#authors      Mestek, A.; Hurley, J.H.; Bye, L.S.; Campbell, A.D.; Chen,
#journal      Y.; Tian, M.; Liu, J.; Schulman, H.; Yu, L.
#title      J. Neurosci. (1995) 15:2396-2406
          The human mu opioid receptor: modulation of functional
          desensitization by calcium/calmodulin-dependent protein
          kinase and protein kinase C.
#cross-references MUID:95198115
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REFERENCE      A38991
#authors      Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.;
          Griffin, C.A.; Uhl, G.R.
#submission      Submitted to GenBank, August 1994
#accession      A38991
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#authors      Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.;
          Griffin, C.A.; Uhl, G.R.
#journal      FEBS Lett. (1994) 338:217-222
#title      Human mu opiate receptor. cDNA and genomic clones,
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#accession      S41075
#status      nucleic acid sequence not shown
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REFERENCE      S51215
#authors      Bare, L.A.; Mansson, E.; Yang, D.
#journal      FEBS Lett. (1994) 354:213-216
#title      Expression of two variants of the human mu opioid receptor
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#accession      S51215
#status      preliminary
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##residues      387-400 #label BAR

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QY	121	VTECCLQFPDDDYSWWDLFMKICVFIFAFAVIVPVLIIIVCYTIMLRKXVRLLSGSREKD	180
Db	275	nrlritrmvlyvvavfiwcwtpihyivlikalvtipettftqtswhficialgytnscln	334
QY	181	XNLRITRLVLYVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYFCIALGYTNSSLN	240
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DATE	12-Jul-1996	#sequence_revision 26-Jul-1996	#text_change
ACCESSIONS	S65693; S51216		
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#authors	Bare, L.A.; Mansson, E.; Yang, D.		
#submission	Submitted to the EMBL Data Library, July 1994		
#description	Expression of two variants of the human mu opioid receptor mRNA in SK-N-SH cells and human brain.		
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REFERENCE	S51215		
#authors	Bare, L.A.; Mansson, E.; Yang, D.		
#journal	FEBS Lett. (1994) 354:213-216		
#title	Expression of two variants of the human mu opioid receptor mRNA in SK-N-SH cells and human brain.		
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ACCESSIONS		I56517; I57951	
REFERENCE		I56517	Bunzow, J.R.; Zhang, G.; Bouvier, C.; Saez, C.; Ronnekleiv, O.K.; Kelly, M.J.; Grandy, D.K.
#authors		J. Neurochem. (1995) 64:14-24	
#journal		Characterization and distribution of a cloned rat mu-opioid receptor.	
#title		receptor.	
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#authors		Chen, Y.; Westek, A.; Liu, J.; Hurley, J.A.; Yu, L.	
#journal		Mol. Pharmacol. (1993) 44:8-12	
#title		Molecular cloning and functional expression of a mu-opioid receptor from rat brain.	
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DATE		26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996	
ACCESSIONS		I56504	
REFERENCE		I56504	Zastawny, R.L.; George, S.R.; Nguyen, T.; Cheng, R.; Tsatsos, J.; Briones-Urbina, R.; O'Dowd, B.F.
#authors		J. Neurochem. (1994) 62:2099-2105	
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#title	cloning, characterization, and distribution of a mu-opioid receptor in rat brain.				
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DATE 10-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 06-Sep-1996

ACCESSIONS  
REFERENCE S34592; 156571

#authors Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.  
#journal FEBS Lett. (1993) 327:311-314  
#title Primary structures and expression from cDNAs of rat opioid receptor delta- and mu-subtypes.

#accession S34592  
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#authors Aboud, M.E.  
#journal J. Neurosci. Res. (1994) 27:714-719  
#title Molecular cloning and expression of a rat delta opioid receptor from rat brain.

#accession 156571  
#status preliminary; translated from GB/EMBL/DDBJ  
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Proc. Natl. Acad. Sci. U.S.A. (1993) 90:6736-6740  
Cloning and functional comparison of kappa and delta opioid  
receptors from mouse brain.

REFERENCE S37807  
#authors Kieffer, B.L.; Befort, K.; Gavériaux-Ruff, C.; Hirth, C.G.  
#submission submitted to the EMBL Data Library, February 1993  
#accession S37807  
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#authors Bzdega, T.; Chin, H.; Kim, H.; Jung, H.H.; Kozak, C.A.; Klee, W.A.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9305-9309  
#title Regional expression and chromosomal localization of the delta opiate receptor gene.

#cross-references MGI:D:94022364  
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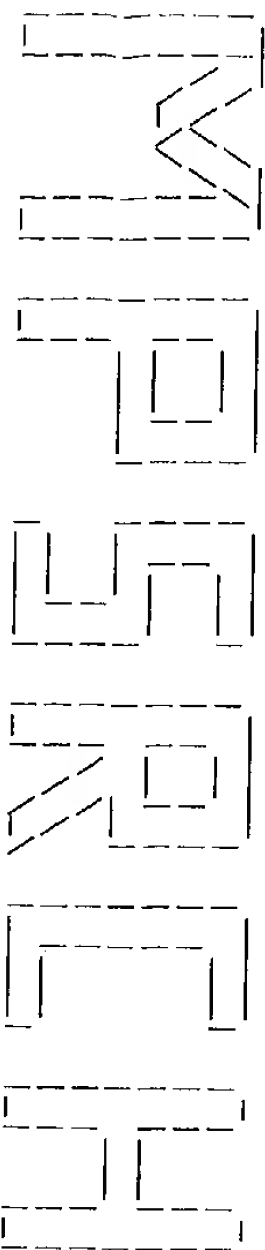
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(TM)

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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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\*\*\*\*\*  
Msrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Aug 26 07:57:57 1997; Maspar time 10.91 Seconds  
573.506 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-292-694A-12  
Description: (1-295) from US08292694A.pep  
Perfect Score: 2229  
Sequence: 1 YTKMKTATNIVIFNLALDA.....NTVQDPAYLREIDGMNKPV 295

Scoring table: PAM 150  
Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot34  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 48.180; Variance 97.876; scale 0.492

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

Result				SUMMARIES	
No.	Score	Query Match Length	ID	Description	Pred. No.
1	2192	98.3	7	OPRK_HUMAN KAPPA-TYPE OPIOID REC	0.00e+00
2	2157	96.8	7	OPRK_CAVPO KAPPA-TYPE OPIOID REC	0.00e+00
3	2136	95.8	7	OPRK_MOUSE KAPPA-TYPE OPIOID REC	0.00e+00
4	2132	95.6	7	OPRK_RAT KAPPA-TYPE OPIOID REC	0.00e+00
5	1524	68.4	7	OPRM_MOUSE MU-TYPE OPIOID RECEPT	1.85e-278
6	1522	68.3	7	OPRM_RAT MU-TYPE OPIOID RECEPT	4.80e-278
7	1520	68.2	7	OPRM_HUMAN MU-TYPE OPIOID RECEPT	1.25e-277
8	1458	65.4	7	OPRD_HUMAN DELTA-TYPE OPIOID REC	8.72e-265
9	1452	65.1	7	OPRD_RAT DELTA-TYPE OPIOID REC	1.52e-263
10	1448	65.0	7	OPRD_MOUSE DELTA-TYPE OPIOID REC	2.01e-262
11	1345	60.3	7	OPRX_RAT PROBABLE OPIOID RECEPT	5.20e-241
12	1343	60.3	7	OPRX_MOUSE PROBABLE OPIOID RECEPT	1.56e-238
13	1331	59.7	7	OPRX_HUMAN PROBABLE OPIOID RECEPT	4.67e-236
14	1319	59.2	7	OPRX_CAVPO PROBABLE OPIOID RECEPT	4.46e-136
15	830	37.2	9	SSRI_MOUSE SOMATOSTATIN RECEPTOR	4.45e-136
16	830	37.2	9	SSRI_HUMAN SOMATOSTATIN RECEPTOR	4.45e-136
17	830	37.2	9	SSRI_RAT SOMATOSTATIN RECEPTOR	2.99e-133
18	822	36.9	9	SSRI_MOUSE SOMATOSTATIN RECEPTOR	4.84e-132
19	816	36.6	9	SSRI_HUMAN SOMATOSTATIN RECEPTOR	8.25e-128
20	810	36.3	9	SSRI_MOUSE SOMATOSTATIN RECEPTOR	8.25e-128
21	789	35.4	9	SSRI_BOVIN SOMATOSTATIN RECEPTOR	8.25e-128
22	789	35.4	9	SSRI_PIG SOMATOSTATIN RECEPTOR	8.25e-128

23	788	35.4	9	SSR2_RAT SOMATOSTATIN RECEPTOR	1.31e-127
24	785	35.2	9	SSR2_MOUSE SOMATOSTATIN RECEPTOR	5.26e-127
25	780	35.0	9	SSR2_HUMAN SOMATOSTATIN RECEPTOR	5.34e-126
26	736	33.0	4	GPR8_HUMAN PROBABLE G PROTEIN-CO	3.65e-117
27	683	30.6	9	SSR3_HUMAN SOMATOSTATIN RECEPTOR	1.44e-106
28	676	30.3	9	SSR5_HUMAN SOMATOSTATIN RECEPTOR	3.58e-105
29	668	30.0	9	SSR5_RAT SOMATOSTATIN RECEPTOR	1.40e-103
30	661	29.7	4	GPR7_HUMAN PROBABLE G PROTEIN-CO	3.46e-102
31	601	27.0	4	SSR3_RAT SOMATOSTATIN RECEPTOR	2.70e-90
32	599	26.9	9	SSR3_MOUSE SOMATOSTATIN RECEPTOR	6.70e-90
33	545	24.5	4	GALR_HUMAN GALANIN RECEPTOR (GAL	2.77e-79
34	496	22.3	2	CKR1_HUMAN C-C CHEMOKINE RECEPTO	9.81e-70
35	496	22.3	359	1 AG2R_CANPA TYPE-1 ANGIOTENSIN II	9.81e-70
36	490	22.0	1	AG22_MOUSE TYPE-2 ANGIOTENSIN II	1.43e-68
37	488	21.9	363	1 AGG2_HUMAN TYPE-2 ANGIOTENSIN II	3.49e-68
38	486	21.8	359	1 AG2R_HUMAN TYPE-1A ANGIOTENSIN I	8.50e-68
39	483	21.8	363	1 AG22_RAT TYPE-2 ANGIOTENSIN II	8.50e-68
40	481	21.7	359	1 AG2R_PIG TYPE-1 ANGIOTENSIN II	3.24e-67
41	481	21.6	359	1 AG2R_RABIT TYPE-1 ANGIOTENSIN II	7.89e-67
42	481	21.6	359	1 AG2S_RAT TYPE-1B ANGIOTENSIN I	7.89e-67
43	476	21.4	359	1 AG2S_MOUSE TYPE-1B ANGIOTENSIN I	7.30e-66
44	475	21.3	359	1 AG2R_MOUSE TYPE-1A ANGIOTENSIN I	1.14e-65
45	475	21.3	359	1 AG2R_BOVIN TYPE-1 ANGIOTENSIN II	1.14e-65

ALIGNMENTS

RESULT 1  
ID OPRK\_HUMAN STANDARD; PRT; 380 AA.  
AC P41145;  
DT 01-FEB-1995 (REL. 31, CREATED)  
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).  
GN OPRK1 OR OPRK.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RX MEDLINE; 94338360.  
RA MANSSON E., BARE L.A., YANG D.;  
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:1431-1437(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RX MEDLINE; 95350200.  
RA SIMONIN F., GAVERIAUS-RUFF C., BEFORT K., LANNES B., MICHELETTI G.,  
RA MATTEI M.-G., CHARON G., BLOCH B., KIEFFER B.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 92:7006-7010(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE; 95174504.  
RA ZHU J., CHEN C., XUE J.C., KUNAPULI S., DERIEL J.K., LIU-CHEN L.-Y.;  
RL LIFE SCI. 56:201-207(1995).  
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR  
FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF  
AUTONOMIC AND ENDOCRINE FUNCTIONS.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; U11053; G532060; -;  
DR EMBL; U17298; G596070; -;  
DR EMBL; L37362; G722618; -;  
DR PIR; JC2338; JC2338.  
DR MIM; 165196; -;  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR.  
DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 59 85 1 (POTENTIAL).

FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 96 117 2 (POTENTIAL).  
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 133 154 3 (POTENTIAL).  
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 174 196 4 (POTENTIAL).  
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 223 247 5 (POTENTIAL).  
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 276 299 6 (POTENTIAL).  
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 312 333 7 (POTENTIAL).  
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 131 210 BY SIMILARITY.  
FT LIPID 345 345 PALMITATE (POTENTIAL).  
FT CARBOHYD 25 25 POTENTIAL.  
FT CARBOHYD 39 39 POTENTIAL.  
FT CONFLICT 2 2 E -> D (IN REF. 2 AND 3).  
SQ SEQUENCE 380 AA; 42659 MW; 1980629E CRC32;

Query Match 98.3%; Score 2192; DB 7; Length 380;  
Best Local Similarity 97.6%; Pred. No. 0.00e+00;  
Matches 288; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladalvtltmpfgstvylnmswpfgdvjckivisidyymfts1 146  
QY 1 ytkmktatniyifnlaladalvtltmpfgstvylnmswpfgdvjckivisidyymfts1 60  
Db 147 ftltmsvdyriavchpvpkaldfrtprlkakiniiciwlsssvgisaiilggtkvredvd 206  
QY 61 ftltmsvdyriavchpvpkaldfrtprlkakiniiciwlsssvgisaiilggtkvredvd 120  
Db 207 iiecslqfpdddysswdlfmkicvtfafvfpvlliiivcytlmlrlkxvrlslgsrekd 266  
QY 121 viecclofpdddysswdlfmkicvtfafvfpvlliiivcytlmlrlkxvrlslgsrekd 180  
Db 267 nrlrritrlvavvavfllcwtpihifilvealgstshstaalssyfficialgytnssl 326  
QY 181 xnlrritrlvavvavfllcwtpihifilvealgstshstaalssyfficialgytnssl 240  
Db 327 pilyaafidenfkrcfrdfcfplkmmersgtsrvntvqdpaylrldgm-nkpv 380  
QY 241 pilyaafidenfkrcfrdfcfplkmmersgtsrvntvqdpaylrldgm-nkpv 295

RESULT 2  
ID OPRK\_CAVPO STANDARD; PRT; 380 AA.  
AC P41144;  
DT 01-FEB-1995 (REL. 31, CREATED)  
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).  
OS CAVIA PORCELLUS (GUINEA PIG).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HARTLEY; TISSUE=BRAIN;  
RX MEDLINE; 94224825.  
RA XIE G.X., MENG F., MANSOUR A., THOMPSON R.C., HOVERSTEN M.T.,  
RA GOLDSTEIN A., WATSON S.J., AKIL H.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 91:3779-3783(1994).  
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR  
FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF  
AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; U04092; G476107; -.  
DR GCRDE; GCR\_0991; -.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.

FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 59 85 1 (POTENTIAL).  
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 96 117 2 (POTENTIAL).  
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 133 154 3 (POTENTIAL).  
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 174 196 4 (POTENTIAL).  
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 223 247 5 (POTENTIAL).  
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 276 299 6 (POTENTIAL).  
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 312 333 7 (POTENTIAL).  
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 131 210 BY SIMILARITY.  
FT LIPID 345 345 PALMITATE (POTENTIAL).  
FT CARBOHYD 25 25 POTENTIAL.  
FT CARBOHYD 39 39 POTENTIAL.  
SQ SEQUENCE 380 AA; 42736 MW; F9F34C4C CRC32;

Query Match 96.8%; Score 2157; DB 7; Length 380;  
Best Local Similarity 94.6%; Pred. No. 0.00e+00;  
Matches 279; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladalvtltmpfgstvylnmswpfgdvjckivisidyymfts1 146  
QY 1 ytkmktatniyifnlaladalvtltmpfgstvylnmswpfgdvjckivisidyymfts1 60  
Db 147 ftltmsvdyriavchpvpkaldfrtprlkakiniiciwlsssvgisaiilggtkvredvd 206  
QY 61 ftltmsvdyriavchpvpkaldfrtprlkakiniiciwlsssvgisaiilggtkvredvd 120  
Db 207 iiecslqfpdddysswdlfmkicvtfafvfpvlliiivcytlmlrlkxvrlslgsrekd 266  
QY 121 viecclofpdddysswdlfmkicvtfafvfpvlliiivcytlmlrlkxvrlslgsrekd 180  
Db 267 nrlrritrlvavvavfllcwtpihifilvealgstshstaalssyfficialgytnssl 326  
QY 181 xnlrritrlvavvavfllcwtpihifilvealgstshstaalssyfficialgytnssl 240  
Db 327 pilyaafidenfkrcfrdfcfplkmmersgtsrvntvqdpaylrldgm-nkpv 380  
QY 241 pilyaafidenfkrcfrdfcfplkmmersgtsrvntvqdpaylrldgm-nkpv 295

RESULT 3  
ID OPRK\_MOUSE STANDARD; PRT; 380 AA.  
AC P33534;  
DT 01-FEB-1994 (REL. 28, CREATED)  
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1) (MSL-1).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE; 93342064.  
RA YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,  
RA BELT G.I.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95100967.  
RA NISHI M., TAKESHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;  
RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95251663.  
RA LIU H.C., LU S., AUGUSTIN L.B., FELSHEIM R.F., CHEN H.C.,  
RA LOH H.H., WEI L.N.;



RL BIOCHEM. BIOPHYS. RES. COMMUN. 209:639-647(1995).  
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR  
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF  
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: BRAIN (NEOCORTEX, HIPPOCAMPUS, AMYGDALA,  
CC MEDIAL HABENULA, HYPOTHALAMUS, LOCUS CERULEUS, AND PARABRACHIAL  
CC NUCLEUS).  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; L11065; G348249; -.  
DR EMBL; D31665; G808876; -.  
DR EMBL; D31663; G808876; JOINED.  
DR EMBL; D31664; G808876; JOINED.  
DR EMBL; S77872; G998532; -.  
DR EMBL; S77868; G998532; JOINED.  
DR EMBL; S77869; G998532; JOINED.  
DR PIR; A48227; A48227.  
DR GCRDB; GCR\_0635; -.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 59 85 1 (POTENTIAL).  
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 96 117 2 (POTENTIAL).  
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 133 154 3 (POTENTIAL).  
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 174 196 4 (POTENTIAL).  
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 223 247 5 (POTENTIAL).  
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 276 299 6 (POTENTIAL).  
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 312 333 7 (POTENTIAL).  
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 131 210 BY SIMILARITY.  
FT LIPID 345 345 PALMITATE (POTENTIAL).  
FT CARBOHYD 25 25 POTENTIAL.  
FT CARBOHYD 39 39 POTENTIAL.  
FT CONFLICT 211 211 S -> L (IN REF. 2 AND 3).  
FT CONFLICT 231 231 F -> V (IN REF. 2 AND 3).  
SQ SEQUENCE 380 AA; 42652 MW; C6F33212 CRC32;  
Query Match 95.8%; Score 2136; DB 7; Length 380;  
Best Local Similarity 92.9%; Pred. No. 0.00e+00;  
Matches 274; Conservative 13; Mismatches 7; Indels 1; Gaps 1;  
Db 87 ytkmktatniyifnlaladalvtltmpfgsavylnmswpfgdvckivisidyymftsi 145  
QY 1 YTKMKTATNIYIFNLALDALVTTTLPFQSTVYLMNSWPFQDYLCKIVISIDYTNMFTSI 60  
Db 147 ftltmsvdryiavchpykaldfrtbpkakinicivllassvgisaivlgtkvredvd 206  
QY 61 FTLTMSVDRIYAVCHPYKALDFRTPLKAKIINICIVLSSSVGISAIVLGTRVEDVD 120  
Db 207 viecslqfpddegswdlfmkicvfvafavipvllivcytlmlrlksvrlisgsredk 266  
QY 121 VIECSLQFPDDDSWDLFMKICVFIFAFAVIPVLLIIVCYTLMILRLKXVRLISGSREKD 180  
Db 267 nllrritklivvvavfiicwtpihifilvealgstshstaalssyyfcialgytnssln 326  
QY 181 XNLRITRLVLVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLN 240  
Db 327 pvllyafldenfkrcfrdcfpikmrmersgtsturnvtvqdpasmrdvgm-nkpv 380  
QY 241 PVLlyAFldENfKrcFRdcFPikMrmERSgtstURnvtVqDPaSMrDvgM-nKpV 295  
RESULT 4  
ID OPERK\_RAT STANDARD; PRI; 380 AA.  
AC P34975;

DT 01-FEB-1994 (REL. 28, CREATED)  
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).  
GN KOR-D.  
OS RATTUS NORVEGICUS (RAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE; 94059008.  
RA CHEN Y., MESTER A., LIU J., YU L.,  
RL BIOCHEM. J. 295:625-628(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 93374033.  
RA MINAMI M., TOYA T., KATAO Y., MAEKAWA K., NAKAMURA S., ONOGI T.,  
RA KANEKO S., SATOH M.,  
RL FEBS LETT. 329:291-295(1993).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;  
RX MEDLINE; 94059009.  
RA LI S., ZHU J., CHEN C., CHEN Y.-W., DERIEL J.K., ASHEY B.,  
RA LIU-CHEN L.-Y.,  
RL BIOCHEM. J. 295:629-633(1993).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;  
RX MEDLINE; 94052210.  
RA MENG F., XIE G.-X., THOMPSON R.C., MANSOUR A., GOLDSTEIN A.,  
RA WATSON S.J., AKIL H.,  
RL PROC. NATL. ACAD. SCI. U.S.A. 90:9954-9958(1993).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WISTAR; TISSUE=BRAIN;  
RX MEDLINE; 93380575.  
RA NISHI M., TAKESHIMA H., FUKUDA K., KATO S., MORI K.,  
RL FEBS LETT. 330:77-80(1993).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY;  
RX MEDLINE; 95204422.  
RA YAKOVLEV A.G., KRUEGER K.E., FADEN A.I.,  
RL J. BIOL. CHEM. 270:6421-6424(1995).  
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR  
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF  
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; L22001; G409237; -.  
DR EMBL; D16829; G404116; -.  
DR EMBL; L22536; G425189; -.  
DR EMBL; U00442; G403487; -.  
DR EMBL; D16534; G415310; -.  
DR EMBL; U17995; G727260; -.  
DR EMBL; U17993; G727260; JOINED.  
DR EMBL; U17994; G727260; JOINED.  
DR PIR; S36143; S36143.  
DR PIR; S38825; S38825.  
DR GCRDB; GCR\_0636; -.  
DR GCRDB; GCR\_0724; -.  
DR GCRDB; GCR\_0790; -.  
DR GCRDB; GCR\_0804; -.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 59 85 1 (POTENTIAL).  
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 96 117 2 (POTENTIAL).

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FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 154 3 (POTENTIAL).
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
FT DISULFID 131 210 BY SIMILARITY.
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 25 25 POTENTIAL.
FT CARBOHYD 39 39 POTENTIAL.
FT CONFLICT 42 42 V -> L (IN REF. 2).
FT CONFLICT 345 345 C -> Y (IN REF. 3).
SQ SEQUENCE 380 AA; 42688 MW; EE858A46 CRC32;
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Query Match 95.6%; Score 2132; DB 7; length 380;  
Best Local Similarity 92.5%; Pred. No. 0.00e+00;  
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

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Db 87 ytkmktatniyifnladalavttttmpfgsavylnmswpfgdvlickivisidyymftstl 146
QY 1 ytkmktatniyifnladalavttttmpfgsavylnmswpfgdvlickivisidyymftstl 60

Db 147 ftltmsvdyriavchpvpkaldfrtprkakiniiciwllssvgisaivlggtkvredvd 206
QY 61 ftltmsvdyriavchpvpkaldfrtprkakiniiciwllssvgisaivlggtkvredvd 120

Db 207 vlcslqfddeswldlrmkicvfaiafvipvliivcytlmlrlksvrlsgrskd 266
QY 121 viecclqfppddyswmdlrmkicvfaiafvipvliivcytlmlrlksvrlsgrskd 180

Db 267 nlrtriklvavavfiicwtpihifilvealgstshststavlssyfcialgytnssln 326
QY 181 xnlrritrlvlyvavfvvcwtpihifilvealgstshststavlssyfcialgytnssln 240

Db 327 pvllyafldenfricfrdfcfrpikmmergstnrvntvqdpasmrdvsgm-nkpy 380
QY 241 pilyafldenfricfrdfcfrpikmmergstnrvntvqdpasmrdvsgm-nkpy 295
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RESULT 5
ID OPRM_MOUSE STANDARD; PRT; 398 AA.
AC P42865;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE MU-TYPE OPIOID RECEPTOR (MOR-1).
GN MOR.
OS MUS. MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=LIVER;
RX MEDLINE; 94377496.
RA MIN B.H., AUGUSTIN L.B., FELSHEIM R.F., FUCHS J.A., LOH H.H.;
RL PROC. NATL. ACAD. SCI. U.S.A. 91:9081-9085(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 95377399.
RA ROSSI G.C., PAN Y.X., BROWN G.P., PASTERNAK G.W.;
RL FEBS LETT. 369:192-196(1995).
CC -I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR BETA-ENDOPHIN.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U10561; G565069; -.
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DR EMBL; U10558; G565069; JOINED.
DR EMBL; U10559; G565069; JOINED.
DR EMBL; U10560; G565069; JOINED.
DR EMBL; U26915; G1055231; -.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 64 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 65 94 1 (POTENTIAL).
FT DOMAIN 95 103 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 104 121 2 (POTENTIAL).
FT DOMAIN 122 143 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 163 3 (POTENTIAL).
FT DOMAIN 164 193 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 194 209 4 (POTENTIAL).
FT DOMAIN 210 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 257 5 (POTENTIAL).
FT DOMAIN 258 280 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 281 303 6 (POTENTIAL).
FT DOMAIN 304 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 328 7 (POTENTIAL).
FT DOMAIN 329 398 CYTOPLASMIC (POTENTIAL).
FT DISULFID 140 217 BY SIMILARITY.
FT LIPID 351 351 PALMITATE (POTENTIAL).
FT CARBOHYD 9 9 POTENTIAL.
FT CARBOHYD 31 31 POTENTIAL.
FT CARBOHYD 38 38 POTENTIAL.
SQ SEQUENCE 398 AA; 44421 MW; C0211489 CRC32;
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Query Match 68.4%; Score 1524; DB 7; length 398;  
Best Local Similarity 65.7%; Pred. No. 1.85e-278;  
Matches 190; Conservative 47; Mismatches 48; Indels 4; Gaps 4;

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Db 96 ytkmktatniyifnladalavttttmpfgsvnylmgtwfpnglickivisidyymftstl 155
QY 1 ytkmktatniyifnladalavttttmpfgsvnylmgtwfpnglickivisidyymftstl 60

Db 156 ftltmsvdyriavchpvpkaldfrtprkakiniiciwllssvgisaivlggtkvredvd 214
QY 61 ftltmsvdyriavchpvpkaldfrtprkakiniiciwllssvgisaivlggtkvredvd 120

Db 215 -idctltfshptv-ywenllkicvfaiafvipvliivcyglmrlksvrlsgrskd 272
QY 121 viecclqfppddyswmdlrmkicvfaiafvipvliivcytlmlrlksvrlsgrskd 180

Db 273 nlrtriklvavavfiicwtpihifilvealgstshststavlssyfcialgytnssln 332
QY 181 xnlrritrlvlyvavfvvcwtpihifilvealgstshststavlssyfcialgytnssln 240

Db 333 pvllyafldenfricfrdfcfrpikmmergstnrvntvqdpasmrdvsgm-nkpy 381
QY 241 pilyafldenfricfrdfcfrpikmmergstnrvntvqdpasmrdvsgm-nkpy 288
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RESULT 6
ID OPRM_RAT STANDARD; PRT; 398 AA.
AC P33535;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE MU-TYPE OPIOID RECEPTOR (MOR-1) (OPIOID RECEPTOR B) (MOR1).
GN MOR-B.
OS RATUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 93351652.
RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;
RL FEBS LETT. 327:311-314(1993).
RN [2]
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R2 SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 94052137.
RA WANG J.-B., IMAI Y., EPLER M.C., GREGOR P., SPIVAK C., UHL G.R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 90:10230-10234(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 93341493.
RA CHEN Y., MESTEK A., LIU J., HURLEY J.A., YU L.;
RL MOL. PHARMACOL. 44:8-12(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RA BUNZOW J.R., GRANDY D.K., KELLY M.;
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=OLFACTORY BULB;
RX MEDLINE; 94059560.
RA THOMPSON R.C., MANSOUR A., AKIL H., WATSON S.J.;
RL NEURON 11:903-913(1993).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR BETA-ENDORPHIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN, WITH HIGH CONCENTRATIONS IN THE
CC BRAINSTEM AND CEREBRUM. NOT DETECTED IN CEREBELLUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; D16349; G391867; -.
DR EMBL; L20684; G409150; -.
DR EMBL; L13069; G348251; -.
DR EMBL; U02083; G403574; -.
DR EMBL; L22455; G437672; -.
DR PIR; S34593; S34593.
DR GCRDB; GCR_0633; -.
DR GCRDB; GCR_0637; -.
DR GCRDB; GCR_0639; -.
DR GCRDB; GCR_0640; -.
DR GCRDB; GCR_0644; -.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 64 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 65 94 1 (POTENTIAL).
FT DOMAIN 95 103 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 104 121 2 (POTENTIAL).
FT DOMAIN 122 143 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 163 3 (POTENTIAL).
FT DOMAIN 164 193 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 194 209 4 (POTENTIAL).
FT DOMAIN 210 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 257 5 (POTENTIAL).
FT DOMAIN 258 280 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 281 303 6 (POTENTIAL).
FT DOMAIN 304 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 328 7 (POTENTIAL).
FT DOMAIN 329 398 CYTOPLASMIC (POTENTIAL).
FT DISULFID 140 217 BY SIMILARITY.
FT LIPID 351 351 PALMITATE (POTENTIAL).
FT CARBOHYD 9 9 POTENTIAL.
FT CARBOHYD 31 31 POTENTIAL.
FT CARBOHYD 38 38 POTENTIAL.
FT CARBOHYD 46 46 POTENTIAL.
FT CARBOHYD 53 53 POTENTIAL.
FT CONFLICT 245 245 V -> I (IN REF. 3 AND 4).
SQ SEQUENCE 398 AA; 44494 MW; 2C21013D CRC32;

Query Match 68.3%; Score 1522; DB 7; Length 398;
Best Local Similarity 66.1%; Pred. No. 4.80e-278;
Matches 191; Conservative 45; Mismatches 49; Indels 4; Gaps 4;
Db 96 ytkmktatniyifnlaladatatstlpfgsvnyimgtwpfgtllickivisidyymftsi 155

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QY 1 ytkmktatniyifnlaladalttmtpfqstvytlmnswpfgdylckivisidyymftsi 60
Db 156 fltctmsvdryiavchpvykalditprnakivncwnllssaiglpvmfmatkyrgg-s 214
QY 61 ftltmmsvdryiavchpvykaldertplkakiiinicllwllssvgsaivlvgtkvreyd 120
Db 215 -ldctltfsbptw-ywenllkicvfifafimpvllitvcyglmllrlksvrmlsgsked 272
QY 121 vteclqfpdddysswmdlrmkicvfiFAFVlPVLllyCYTLMLlRLKXVRLlSGSREKD 180
Db 273 nlrirtrmvlvvaavflvcwtpibhiylikalitpetttqtswhfciatgynscln 332
QY 181 xnlrritrlylvvaavfvcwtpihifilvealgssthsstaaalssyfciaigtynssln 240
Db 333 pviyaflidenfkrcfrefcelpststieqgnstrvrgntrehpstantvd 381
QY 241 pilyaflDENfKRCfRDFCFPLKMXMERKXSTSVR-NTVQDPAYLREID 288

RESULT 7
ID OPRM_HUMAN STANDARD; PRI; 400 AA.
AC P35372;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE MU-TYPE OPIOID RECEPTOR (MOR-1).
GN OPRM1 OR MOR1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 94139928.
RA WANG J.-B., JOHNSON P.S., PERISCO A.M., HAWKINS A.L., GRIFFIN C.A.,
RA UHL G.R.;
RL FEBS LETT. 338:217-222(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA MESTEK A. JR., HURLEY J.H., BYE L.S., CAMPBELL A., TIAN M.,
RA CHEN Y., YU L.;
RL SUBMITTED (XXX-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR BETA-ENDORPHIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; L25119; G452073; -.
DR EMBL; L29301; G459832; -.
DR GCRDB; GCR_0885; -.
DR GCRDB; GCR_0966; -.
DR MIM; 600018; -.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 66 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 67 96 1 (POTENTIAL).
FT DOMAIN 97 105 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 106 123 2 (POTENTIAL).
FT DOMAIN 124 145 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 146 165 3 (POTENTIAL).
FT DOMAIN 166 195 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 196 211 4 (POTENTIAL).
FT DOMAIN 212 236 5 (POTENTIAL).
FT TRANSMEM 237 259 6 (POTENTIAL).
FT DOMAIN 260 282 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 283 305 7 (POTENTIAL).
FT DOMAIN 306 313 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 314 330 7 (POTENTIAL).
FT DOMAIN 331 400 CYTOPLASMIC (POTENTIAL).
FT DISULFID 142 219 BY SIMILARITY.

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FT LIPID 353 353 PALMITATE (POTENTIAL).  
FT CARBOHYD 9 9 POTENTIAL.  
FT CARBOHYD 12 12 POTENTIAL.  
FT CARBOHYD 33 33 POTENTIAL.  
FT CARBOHYD 40 40 POTENTIAL.  
FT CARBOHYD 48 48 POTENTIAL.  
FT CARBOHYD 51 51 N -> D (IN REF. 2).  
FT CONFLICT 234 234 V -> L (IN REF. 2).  
SQ SEQUENCE 400 AA; 44764 MW; 3F40D610 CRC32;

Query Match 68.2%; Score 1520; DB 7; Length 400;  
Best Local Similarity 67.1%; Pred. No. 1.25e-277;  
Matches 188; Conservative 43; Mismatches 46; Indels 3; Gaps 3;

Db 98 ytkmktatniyifnlaladalatstlpfgsvnylmgtpfgtlckivisidyymftsi 157  
1 ytkmktatniyifnlaladalatstlpfgsvnylmgtpfgtlckivisidyymftsi 60  
Db 158 ftlctmsvdryiaavchpvpkaldfrtprnakilnvcnwllssaiglpmfmatkkyrgg-s 216  
61 ftltmmsvdryiaavchpvpkaldfrtprnakilnvcnwllssaiglpmfmatkkyrgg-s 120  
Db 217 -idctltfshptw-ywenlvkicvffafimpylittvcyglmllrlksvmlsgsked 274  
121 viecclqfpddyswmdlfmkicvffafimpylittvcyglmllrlksvmlsgsked 180  
Db 275 nrlrltmvlyvvaavfivcwtpbhiyvlkalvltipettftqtswhficialgytnscin 334  
181 xnlrritrlvlyvvaavfivcwtpbhiyvlkalvltipettftqtswhficialgytnscin 240  
Db 335 pvllyafldenfkrcfrfcipstsnieqgnstrirgntrd 374  
241 pilyafldenfkrcfrfcipstsnieqgnstrirgntrd 280

RESULT 8  
ID OPND HUMAN STANDARD; PRT; 372 AA.

AC P41143;  
DT 01-FEB-1995 (REL. 31, CREATED)  
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1).  
GN OPND1 OR OPND.  
OS HOMO SAPIENS (HUMAN).  
OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=CEREBRAL CORTEX, AND STRIATUM;  
RX MEDLINE; 94260835.  
RA KANAP R.J., MALATYNSKA E., FANG L., LI X., BABIN E., NGUYEN M.,  
RA SANTORO G., VARGA E.V., HRUBY V.J., ROESKE W.R., YAMAMURA H.I.;  
RL LIFE SCI. 54:463-469(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95107267.  
RA SIMONIN F., BEFORT K., GAVERIAUX-RUEF C., MATTHES H., NAPPET V.,  
RA LANNES B., MICHELETTI G., KIEFFER B.;  
RL MOL. PHARMACOL. 46:1015-1021(1994).  
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY  
STERESELECTIVE. RECEPTOR FOR ENKEPHALINS.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; U07882; G497314; -.  
DR EMBL; U10504; E162517; -.  
DR MIM; 165195; -.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 46 75 1 (POTENTIAL).  
FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 85 102 2 (POTENTIAL).  
FT DOMAIN 103 124 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 125 144 3 (POTENTIAL).  
FT DOMAIN 145 174 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 175 190 4 (POTENTIAL).  
FT TRANSMEM 191 215 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 216 238 5 (POTENTIAL).  
FT DOMAIN 239 261 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 262 284 6 (POTENTIAL).  
FT DOMAIN 285 293 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 294 310 7 (POTENTIAL).  
FT DOMAIN 311 372 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 18 18 POTENTIAL.  
FT CARBOHYD 33 33 BY SIMILARITY.  
FT DISULFID 121 198 PALMITATE (POTENTIAL).  
FT LIPID 333 333 F -> C (IN REF. 2).  
FT CONFLICT 27 27 PG -> AR (IN REF. 2).  
FT CONFLICT 40 41 P -> A (IN REF. 2).  
FT CONFLICT 348 348 R -> A (IN REF. 2).  
SQ SEQUENCE 372 AA; 40450 MW; CFF92985 CRC32;

Query Match 65.4%; Score 1458; DB 7; Length 372;  
Best Local Similarity 69.2%; Pred. No. 8.72e-265;  
Matches 180; Conservative 43; Mismatches 33; Indels 4; Gaps 4;

Db 77 ytkmktatniyifnlaladalatstlpfqsakylmetwpgellckavlsidyymftsi 136  
1 ytkmktatniyifnlaladalatstlpfqsakylmetwpgellckavlsidyymftsi 60  
Db 137 ftltmmsvdryiaavchpvpkaldfrtprnakilnvcnwllssaiglpmfmatkkyrgg-s 195  
61 ftltmmsvdryiaavchpvpkaldfrtprnakilnvcnwllssaiglpmfmatkkyrgg-s 120  
Db 196 vv-cmlqfppsw-ywdltvkicvflfaivpilitvcyglmllrlksvmlsgsked 253  
121 viecclqfpddyswmdlfmkicvffafimpylittvcyglmllrlksvmlsgsked 180  
Db 254 rslrltmvlyvvaavfivcwtpbhiyvlkalvltipettftqtswhficialgytnscin 313  
181 xnlrritrlvlyvvaavfivcwtpbhiyvlkalvltipettftqtswhficialgytnscin 239  
Db 314 npvlyafldenfkrcfrqlc 333  
240 npilyafldenfkrcfrqlc 259

RESULT 9  
ID OPND RAT STANDARD; PRT; 372 AA.

AC P33533;  
DT 01-FEB-1994 (REL. 28, CREATED)  
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1) (OPIOID RECEPTOR A).  
GN ROR-A.  
OS RATTUS NORVEGICUS (RAT).  
OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE; 93351652.  
RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;  
RL FEBS LETT. 327:311-314(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;  
RX MEDLINE; 94322412.  
RA ABOOD M.E., NOEL M.A., FARNSWORTH J.S., TAO Q.;  
RL J. NEUROSCI. RES. 37:714-719(1994).  
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY  
STERESELECTIVE. RECEPTOR FOR ENKEPHALINS.



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CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; D16348; G391865; -.
DR EMBL; U00475; G514211; -.
DR PIR; S34592; S34592.
DR GCRDB; GCR_0638; -.
DR GCRDB; GCR_0805; -.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR.
DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 75 1 (POTENTIAL).
FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 85 102 2 (POTENTIAL).
FT DOMAIN 103 124 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 125 144 3 (POTENTIAL).
FT DOMAIN 145 174 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 175 190 4 (POTENTIAL).
FT DOMAIN 191 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 238 5 (POTENTIAL).
FT DOMAIN 239 261 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 262 284 6 (POTENTIAL).
FT TRANSMEM 285 293 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 294 310 7 (POTENTIAL).
FT DOMAIN 311 372 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 18 18 POTENTIAL.
FT CARBOHYD 33 33 POTENTIAL.
FT DISULFID 121 198 BY SIMILARITY.
FT LIPID 333 333 PALMITATE (POTENTIAL).
SQ SEQUENCE 372 AA; 40449 MW; 59F5EE50 CRC32;

Query Match 65.1%; Score 1452; DB 7; Length 372;
Best Local Similarity 68.8%; Pred. No. 1.52e-263;
Matches 179; Conservative 44; Mismatches 33; Indels 4; Gaps 4;

Db 77 ytklktatniyifnlaladalatstlpfqsakylmetwpgellckavlsidymnftsi 136
QY 1 ytkmktatniyifnlaladalatstlpfqsakylmetwpgellckavlsidymnftsi 60

Db 137 ftltmmsvdyriavchpvcakaldftrtpakaliniiciwlvlasgyvplmvmavtqprdga- 195
QY 61 ftltmmsvdyriavchpvcakaldftrtpakaliniiciwlvlasgyvplmvmavtqprdga- 120

Db 196 vv-cltqfppsw-ywdvtvkicvlfafvvpillitvcygmllrlsvllsgsked 253
QY 121 vtecltqfppddyswvdlmklcveifaavivpvlititvctlmilrlkxvrlsgsrexk 180

Db 254 tslrritmvlvvvgafvvcvapihifivwtlvdinrrdpvlvaahlciaigyanssl 313
QY 181 xnlrritrvlvvavfvvcvapihifivwtlvdinrrdpvlvaahlciaigyanssl 239

Db 314 npvlyafldenfkrcfqlc 333
QY 240 npllyafldenfkrcfqlc 259

RESULT 10
ID OPD_MOUSE STANDARD; PRT; 372 AA.
AC P32300;

DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1) (K56) (MSL-2).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93101664.
RA KIEFFER B.L., BEBORT K., GAVERIAUX-RUFF C., HIRTH C.G.;
RL PROC. NATL. ACAD. SCI. U.S.A. 89:12048-12052(1992).
RN [2]
RP SEQUENCE FROM N.A.

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RX MEDLINE; 93110361.
RA EVANS C.J., KEITH D.E. JR., MORRISON H., MAGENDZO K., EDWARDS R.H.;
RL SCIENCE 258:1952-1955(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 93342064.
RA YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,
RA BEL G.I.;
RL PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).
RN [4]
RP SEQUENCE FROM N.A.
RA KEITH D.E. JR., ANTON B., EVANS C.J.;
RL PROC. WEST. PHARMACOL. SOC. 36:299-306(1993).
RN [5]
RP SEQUENCE OF 8-372 FROM N.A.
RX MEDLINE; 94022364.
RA BZDEGA T., CHIN H., KIM K., JUNG H.H., KOZAK C.A., KLEE W.A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 90:9305-9309(1993).
RN [6]
RP 3D-STRUCTURE MODELLING.
RX MEDLINE; 97001837.
RA ALKORTA I., LOEW G.H.;
RL PROTEIN ENG. 9:573-583(1996).
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
CC STEREOSPECIFIC. RECEPTOR FOR ENKEPHALINS.
CC -!- TISSUE SPECIFICITY: BRAIN, WITH HIGH CONCENTRATIONS IN THE BASAL
CC GANGLIA AND LIMBIC REGIONS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; L06322; G192943; -.
DR EMBL; L07271; -; NOT_ANNOTATED_CDS.
DR EMBL; L11064; G348247; -.
DR EMBL; S65335; G442326; -.
DR EMBL; S66181; G435782; -.
DR PIR; S37807; S37807.
DR PIR; B48227; B48227.
DR GCRDB; GCR_0229; -.
DR GCRDB; GCR_0493; -.
DR GCRDB; GCR_0634; -.
DR GCRDB; GCR_0842; -.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 75 1 (POTENTIAL).
FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 85 102 2 (POTENTIAL).
FT DOMAIN 103 124 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 125 144 3 (POTENTIAL).
FT DOMAIN 145 174 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 175 190 4 (POTENTIAL).
FT DOMAIN 191 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 238 5 (POTENTIAL).
FT DOMAIN 239 261 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 262 284 6 (POTENTIAL).
FT TRANSMEM 285 293 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 294 310 7 (POTENTIAL).
FT DOMAIN 311 372 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 18 18 POTENTIAL.
FT CARBOHYD 33 33 POTENTIAL.
FT DISULFID 121 198 BY SIMILARITY.
FT LIPID 333 333 PALMITATE (POTENTIAL).
SQ SEQUENCE 372 AA; 40561 MW; 514022F5 CRC32;

Query Match 65.0%; Score 1448; DB 7; Length 372;
Best Local Similarity 68.8%; Pred. No. 1.02e-262;
Matches 179; Conservative 44; Mismatches 33; Indels 4; Gaps 4;

Db 77 ytklktatniyifnlaladalatstlpfqsakylmetwpgellckavlsidymnftsi 136
QY 1 ytkmktatniyifnlaladalatstlpfqsakylmetwpgellckavlsidymnftsi 60

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ID OPRX_MOUSE STANDARD; PRT; 367 AA.
AC P35377;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE PROBABLE OPIOID RECEPTOR (ORGC).
GN
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6N; TISSUE=BRAIN;
RA YASUDA K., JONES E., REISINE T., BELL G.I.;
RL SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95100967.
RA NISHI M., TAKESHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RA MATTHEW H.W.D.;
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RP SEQUENCE OF 1-357 FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RA HALFORD W.P., GEBHARDT B.M., CARR D.J.J.;
RL SUBMITTED (AUG-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: OPIOD RECEPTOR WITH A POTENTIAL ROLE IN MODULATING A
CC NUMBER OF BRAIN FUNCTIONS, INCLUDING INSTINCTIVE BEHAVIOURS AND
CC EMOTIONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS
CC WHICH INHIBITS ADENYLYL CYCLASE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U04952; G440880; -.
DR EMBL; D31667; G808874; -.
DR EMBL; D31666; G808874; JOINED.
DR EMBL; X91813; G1008982; -.
DR EMBL; U14165; G540093; -.
DR GCRDB; GCR 0891; -.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 48 74 1 (POTENTIAL).
FT DOMAIN 75 84 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 85 106 2 (POTENTIAL).
FT DOMAIN 107 121 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 122 143 3 (POTENTIAL).
FT DOMAIN 144 162 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 163 185 4 (POTENTIAL).
FT DOMAIN 186 208 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 209 233 5 (POTENTIAL).
FT DOMAIN 234 261 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 262 285 6 (POTENTIAL).
FT DOMAIN 286 297 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 298 319 7 (POTENTIAL).
FT DOMAIN 320 366 CYTOPLASMIC (POTENTIAL).
FT DISULFID 120 197 BY SIMILARITY.
FT LIPID 331 331 PALMITATE (POTENTIAL).
FT CARBOHYD 21 26 POTENTIAL.
FT CARBOHYD 26 26 POTENTIAL.
FT CARBOHYD 36 36 POTENTIAL.
SQ SEQUENCE 367 AA; 40491 MW; 3F472156 CRC32;
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Query Match 60.3%; Score 1343; DB 7; Length 367;  
Best Local Similarity 62.1%; Pred. No. 5.20e-241;  
Matches 174; Conservative 46; Mismatches 55; Indels 5; Gaps 5;

Db 77 tkmtatniyifnlaladtlvltlfpqgtdllgfwfngalcktvialdyymftstf 136  
|||||

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QY 2 TKMTATNIYIFNLALADALVTTMPFQSTVIYINMSWPFGLCKIVISIDYXNMTSIF 61
Db 137 tlamsvdryvaichpiraldvrtsskagavnavialasvgyvpaimsgaqy-edee- 194
QY 62 TLTMSVDRIYAVCHPYKALDERTPLKAKIINICLTWLLSSVGSISAIVLGITKREDVDY 121
Db 195 ieciveipapqdy-wgvpfa-iciflfsfipvllisvcyslmirrlgrllsgsrekd 252
QY 122 IECCLOFPD-DDYSMDLPMKICVFIFAFAVIVPVLIIIVCYTLMILRLKXVRLSGSREKD 180
Db 253 nlrirtrlvvvavfvgcwtprvqfvlgvglgvpgsetavailrfctalgvnscln 312
QY 181 XNLRIRITLVVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYFCTALGYTNSSLN 240
Db 313 pilyafldenfkacfkfcoasalhremqvsdrvsiakd 352
QY 241 PILYAFLDENFKCFRDFCFPLKMXMERXSTSRVKNTVQD 280
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RESULT 13
ID OPRX_HUMAN STANDARD; PRT; 370 AA.
AC P41146;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PROBABLE 476 POTENTIAL.
FT CARBOHYD 532 532 POTENTIAL.
FT CARBOHYD 540 540 POTENTIAL.
FT CARBOHYD 556 556 POTENTIAL.
FT CARBOHYD 576 576 POTENTIAL.
FT CARBOHYD 623 623 POTENTIAL.
FT CARBOHYD 645 645 POTENTIAL.
FT CARBOHYD 2041 2041 POTENTIAL.
FT CARBOHYD 2077 2077 POTENTIAL.
FT CARBOHYD 2240 2240 POTENTIAL.
FT CARBOHYD 2364 2364 POTENTIAL.
FT CARBOHYD 2789 2789 POTENTIAL.
SQ SEQUENCE 3011 AA; 327197 MW; 0726B84 CRC32;
```

Query Match 95.7%; Score 4322; DB 7; Length 3011;  
Best Local Similarity 92.7%; Pred. No. 0.00e+00;  
Matches 585; Conservative 35; Mismatches 11; Indels 0; Gaps 0;

Db 1027 apitayaqqlrgllgciltsltgrdknqvegevgqvistagqtlatcngvcwtvynag 1086  
QY 1 APTIAYSQQTGRLLGCIITSLTGRDKNOVEGEVQVSTAFQSLATCVNGVCWTVYHGAG 60  
Db 1087 trtiaspkqpvigmytnvdqglvgwpaqgsrsiltpctcgssdlylvtrhadviprrrrg 1146  
QY 61 SKTLAAPKGPITQMTNVDQLVGWPKPGARSLTPCTCGSSDLYLVTRHADVIPYRRRG 120  
Db 1147 dsergslsprpisylyksgsggpllcpgahavgifraavctrgvakavdfigvenletmr 1206  
QY 121 DSRGSLSPRPVSYLKSSGGLLCPFGHAVGIFRAVCTRGVAKAVDFVPESMETMR 180  
Db 1207 spvftdnssppvvpqsfgyahlnaptsgskstkypaayaaggykvlinpsvaatlfga 1266  
QY 181 SPVFTDNSSPPAVPQSFQVAHLHAPTSGSKSTKYPAAAYAQGYKVLVNPVATLGFGA 240  
Db 1267 ymskahgidpnirtgyvrtittgspitystygykfiadggcgsgaydiilicdehstatsi 1326  
QY 241 YMSKAHGIDPNIRIGVYRTITGAPVYTYSTYKFLADGGCGSGAYDIILICDEHSTDSTI 300  
Db 1327 lgiqtlvdaetagarlvlatatpvgsvtyvphnieevalsttgeipfykaiplevik 1386  
QY 301 LGIGTVLDQAEETAGARLVYLATATPVGSVTYVPHNIEVALSNTGEIPFYKAIPLEAIR 360  
Db 1387 ggrhlifchskkkcdelaaklvalglnavayrrglvsviptsgdvvvvatdalmtygtg 1446  
QY 361 GGRHLIFCHSKKCDELAAKLSGLGINAVAYRRGLVSVIPTIGDVVVVATDALMTGYTG 420  
Db 1447 dfdsvidontcvrtqtdvdfslqptfttlettlpqdavsrtrgrgrtgrgkpgiyrfvapge 1506  
|||||

QY 421 DFDVIDCNTCVTFVDFSLDPTFTIETTIVPODAVSRSQRRGTGRGRGIYRVTPE 480

Db 1507 rpsgmfdssvllcecydagcaweltpaetvrlraymntpglpvcqdhlefegvftgtlt 1566

QY 481 RPSGMFDSSVLLCECYDAGCAWYELTPAETSVRLRAYLNTPGLPVCQDHLFEWESVETGLT 540

Db 1567 hidahflsqtksgeenlpylvayqatvcaraqapppswdqmwkclirlikptlhpptpily 1626

QY 541 HIDAHFLSQTKQAGDNFPIYAYQATVCARAQAAPPSPWDQMWKCLIRLKPTLHSGPTPLLY 600

Db 1627 rlgavqneitltlhpvtkyimtcmsadlevvt 1657

QY 601 RLGAVQNEVTLTHPTKYMCMASADLEVVT 631

RESULT 6 STANDARD; PRT; 3011 AA.

ID POLG\_HCVH

AC p27958;

DT 01-AUG-1992 (REL. 23, CREATED)

DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)

DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)

DE GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEIN NS1, NS2, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (NS5)).

DE HEPATITIS C VIRUS (ISOLATE H) (HCV).

OS VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;

OC HCV GROUP VIRUSES.

OC [1]

RN SEQUENCE FROM N.A.

RP MEDLINE; 92052256.

RX INCHAUSPE G., ZEBEDEE S., LEE D.H.H., SUGITANI M., NASOFF M.,

RA PRINCE A.M.;

RA PROC. NATL. ACAD. SCI. U.S.A. 88:10292-10296(1991).

RL -I- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.

CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

CC -I- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.

CC EMBL; M67463; G329738; -.

DR PIR; A36814; GNMVCH.

DR POLYPROTEIN; GLYCOPROTEIN; RNA-DIRECTED RNA POLYMERASE; CORE PROTEIN; COAT PROTEIN; ENVELOPE PROTEIN; HELICASE; ATP-BINDING; TRANSMEMBRANE; NONSTRUCTURAL PROTEIN.

KW INIT\_MET 1 1

FT CHAIN 2 115

FT CHAIN 116 191

FT CHAIN 192 383

FT CHAIN 384 729

FT CHAIN 730 1006

FT CHAIN 1007 1615

FT CHAIN 1616 1862

FT CHAIN 1863 2013

FT CHAIN 2014 3011

FT TRANSMEM 347 369

FT NP\_BIND 1230 1237

FT SITE 1316 1319

FT CARBOHYD 196 196

FT CARBOHYD 209 209

FT CARBOHYD 234 234

FT CARBOHYD 305 305

FT CARBOHYD 417 417

FT CARBOHYD 423 423

FT CARBOHYD 430 430

FT CARBOHYD 448 448

FT CARBOHYD 476 476

FT CARBOHYD 532 532

FT CARBOHYD 540 540

FT CARBOHYD 556 556

FT CARBOHYD 576 576 POTENTIAL.

FT CARBOHYD 623 623 POTENTIAL.

FT CARBOHYD 645 645 POTENTIAL.

FT CARBOHYD 2041 2041 POTENTIAL.

FT CARBOHYD 2240 2240 POTENTIAL.

FT CARBOHYD 2364 2364 POTENTIAL.

FT CARBOHYD 2789 2789 POTENTIAL.

SO SEQUENCE 3011 AA; 327142 MW; 49643481 CRC32;

Query Match 94.5%; Score 4266; DB 7; Length 3011;

Best Local Similarity 91.98; Pred. No. 0.00e+00;

Matches 580; Conservative 38; Mismatches 13; Indels 0; Gaps 0;

Db 1027 apitayaqgtrgligclitsltgrdknqvegevgqlvstatqftlatcinqvcwtyhag 1086

QY 1 ADITAYSQQTRGLIGCLITSLTGRDKNQVEGEVGQVSTATQSFLATCVNGVCWTYHAG 60

Db 1087 tttiaspkpviqlytnvdqdlvgwpapqgsrsltpctcgssdlylvtrhadviprrrg 1146

QY 61 SKTLAAPKGPITQMTYNDQDLVGPMPKPPGARSITPCTCGSSDLYLVTRHADVIPRRRG 120

Db 1147 dsrgslsprisylksgsggpllpctghavglfraavctrvakavdflpvenletmr 1206

QY 121 DSRGSLSPRPVSYLKSGSGGDLCPFGHAVGIFRAVCTRGVAKAVDFVPVESMETMR 180

Db 1207 spvftdnsspavpqsfgvalhnapltsqskstkvpaaayakgkvlvlnpsvaatlgtfga 1266

QY 181 SPVFTDNSSPAVPQSFQVAHLHAPTGSGSKSTKVPAAAYAAQYKVLVLPNSVAATLGFGA 240

Db 1267 ymskahgvdpnirtgvrtiltgspltystygkfladagcsqgaydiliicdechnstatts 1326

QY 241 YMSKAHGIDPNIRITGVRTITGAPVYTYSGKFLADGGCSGAYDIILICDECHSTDSTTI 300

Db 1327 sgltgvlqdaetagarlvlatatppgsvtvshpnievalstgeipfygkaiplevik 1386

QY 301 LGIGTVLQDAETAGARLVLATATPPGSVTVPHPNIEVALSTGEIPFYGKAIPLEAIR 360

Db 1387 ggrhlifchskkkcdelaaklivalqlnavayyrgldvsvipstgsdvvvstdalmtgtg 1446

QY 361 GGRHLIFCHSKKKCDLELAabel= Cys, Arg

FT Misc\_difference 246

FT /label= leu, phe

FT Misc\_difference 263

FT /label= Asp, Asn

FT Misc\_difference 291

FT /label= phe, ser

FT Misc\_difference 311

FT /label= gly, asp

FT Misc\_difference 398

FT /label= ser, arg, gly

FT Misc\_difference 400

FT /label= thr, ala

FT Misc\_difference 405

FT /label= gln, pro, leu

FT Misc\_difference 410

FT /label= lys, arg

FT Misc\_difference 418

FT /label= gly, asp

FT Misc\_difference 430

FT /label= asn, asp

FT Misc\_difference 438

FT /label= phe, leu

FT Misc\_difference 478

FT /label= arg, lys

FT Misc\_difference 759

FT /label= leu, val

FT Misc\_difference 1017

FT /label= ser, asn

FT Misc\_difference 1036

FT /label= thr, ala

FT Misc\_difference 1056

FT /label= glu, asp

FT Misc\_difference 1201



FT /label= Met, Thr  
FT Misc\_difference 1205  
FT /label= Met, Ile  
FT Misc\_difference 1255  
FT /label= Asn, Tyr  
FT Misc\_difference 1263  
FT /label= Gly, Asp  
FT Misc\_difference 1455  
FT /label= Asn, Asp  
FT Misc\_difference 1828  
FT /label= Ala, Thr  
FT Misc\_difference 1895  
FT /label= Gly, Arg  
FT Misc\_difference 1896  
FT /label= Gly, Ile  
FT Misc\_difference 2143  
FT /label= Glu, Val  
FT Misc\_difference 2144  
FT /label= Asp, Glu  
FT Misc\_difference 2462  
FT /label= Cys, Arg  
FT Misc\_difference 2486  
FT /label= Val, Met  
FT Misc\_difference 2488  
FT /label= Lys, Gln  
FT Misc\_difference 2844  
FT /label= Leu, Met  
FT Misc\_difference 2862  
FT /label= Leu, Gln  
FT Misc\_difference 2917  
FT /label= Arg, Leu  
FT Misc\_difference 2968  
FT /label= Ser, Gly  
FT Misc\_difference 2989  
FT /label= Cys, Arg  
FT Misc\_difference 2990  
FT /label= Tyr, Cys  
FT J06105690-A.  
PN J06105690-A.  
PD 19-APR-1994.  
PF 10-MAR-1992; 051885.  
PR 10-MAR-1992; JP-051885.  
PA (KAEN/) KAENNO K.  
DR WPI; 94-163130/20.  
DR N-PSDB; Q63499.  
PT Blood-transmissible non-A non-B hepatitis virus DNA - used for  
PT detection of hepatitis virus  
PS Claim 1; Page 8-20; 22pp; Japanese.  
CC This sequence is encoded by the genome of a blood transmissible non-A,  
CC non-B hepatitis (NANBH) virus. The cDNA sequence was isolated using the  
CC primers given in Q63500-35. The amplified fragments are used in the  
CC detection of hepatitis virus. The target DNA was isolated from serum  
CC of chronically infected NANBH patients who were C100 antibody-positive  
CC and HCV RNA (NS5 region) positive. Reverse transcription-PCR and PCR  
CC were performed on cDNA and the total hum

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Msrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Aug 26 07:54:10 1997; MasPar time 13.34 Seconds  
591.383 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-292-694A-4  
Description: (1-372) from US08292694A.pep  
Perfect Score: 2743  
Sequence: 1 MELVPSARAELOSSPLVNL.....TRERYTACTPSDGGGAAA 372

Scoring table: PAM 150  
Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot34  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 49.691; Variance 96.228; scale 0.516

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2743	100.0	372	7	OPRD_MOUSE	DELTA-TYPE OPIOID REC	0.00e+00
2	2657	96.9	372	7	OPRD_RAT	DELTA-TYPE OPIOID REC	0.00e+00
3	2581	94.1	372	7	OPRD_HUMAN	DELTA-TYPE OPIOID REC	0.00e+00
4	1729	63.0	400	7	OPRM_HUMAN	MU-TYPE OPIOID RECEPTOR	0.00e+00
5	1721	62.7	398	7	OPRM_MOUSE	MU-TYPE OPIOID RECEPTOR	0.00e+00
6	1716	62.6	398	7	OPRM_MOUSE	MU-TYPE OPIOID RECEPTOR	0.00e+00
7	1604	58.5	380	7	OPRK_RAT	KAPPA-TYPE OPIOID REC	0.00e+00
8	1604	58.5	380	7	OPRK_HUMAN	KAPPA-TYPE OPIOID REC	0.00e+00
9	1597	58.2	380	7	OPRK_MOUSE	KAPPA-TYPE OPIOID REC	0.00e+00
10	1592	58.0	380	7	OPRK_MOUSE	KAPPA-TYPE OPIOID REC	0.00e+00
11	1471	53.6	370	7	OPRX_HUMAN	PROBABLE OPIOID RECEPTOR	1.63e-279
12	1463	53.3	367	7	OPRX_RAT	PROBABLE OPIOID RECEPTOR	8.88e-278
13	1460	53.2	367	7	OPRX_MOUSE	PROBABLE OPIOID RECEPTOR	3.98e-277
14	1428	52.1	370	7	OPRX_CAVPO	PROBABLE OPIOID RECEPTOR	3.46e-270
15	1002	36.5	388	9	SSR4_HUMAN	SOMATOSTATIN RECEPTOR	1.94e-173
16	977	35.6	384	9	SSR4_RAT	SOMATOSTATIN RECEPTOR	4.21e-173
17	970	35.4	384	9	SSR4_MOUSE	SOMATOSTATIN RECEPTOR	1.31e-171
18	957	34.9	391	9	SSR1_HUMAN	SOMATOSTATIN RECEPTOR	7.74e-169
19	957	34.9	391	9	SSR1_MOUSE	SOMATOSTATIN RECEPTOR	7.74e-169
20	957	34.9	391	9	SSR1_RAT	SOMATOSTATIN RECEPTOR	7.74e-169
21	892	32.5	369	9	SSR2_PIG	SOMATOSTATIN RECEPTOR	5.18e-155
22	885	32.3	368	9	SSR2_BOVIN	SOMATOSTATIN RECEPTOR	1.59e-153

23	887	32.3	369	9	SSR2_RAT	SOMATOSTATIN RECEPTOR	5.97e-154
24	879	32.0	369	9	SSR2_MOUSE	SOMATOSTATIN RECEPTOR	2.97e-152
25	873	31.8	333	4	GPR8_HUMAN	PROBABLE G PROTEIN-CO	5.57e-151
26	871	31.8	369	9	SSR2_HUMAN	SOMATOSTATIN RECEPTOR	1.48e-150
27	848	30.9	363	9	SSR5_HUMAN	SOMATOSTATIN RECEPTOR	1.10e-145
28	835	30.4	418	9	SSR3_HUMAN	SOMATOSTATIN RECEPTOR	6.20e-143
29	831	30.3	363	9	SSR5_RAT	SOMATOSTATIN RECEPTOR	4.35e-142
30	821	29.9	328	4	GPR7_HUMAN	PROBABLE G PROTEIN-CO	5.64e-140
31	768	28.0	428	9	SSR3_RAT	SOMATOSTATIN RECEPTOR	1.73e-126
32	757	27.6	428	9	SSR3_MOUSE	SOMATOSTATIN RECEPTOR	8.41e-129
33	605	22.1	349	4	GALR_HUMAN	GALANIN RECEPTOR (GAL	8.56e-95
34	569	20.7	355	2	CKR1_HUMAN	C-C CHEMOKINE RECEPTOR	2.25e-87
35	548	20.0	359	1	AG2R_BOVIN	TYPE-1 ANGIOTENSIN II	4.57e-83
36	547	19.9	359	1	AG2R_CANEA	TYPE-1 ANGIOTENSIN II	7.32e-83
37	541	19.7	359	1	AG2R_HUMAN	TYPE-1A ANGIOTENSIN I	1.24e-81
38	536	19.5	359	1	AG2S_RAT	TYPE-1B ANGIOTENSIN I	1.30e-80
39	535	19.5	359	1	AG2R_PIG	TYPE-1 ANGIOTENSIN II	2.09e-80
40	532	19.4	362	1	AG2R_XENLA	TYPE-1-LIKE ANGIOTENS	8.55e-80
41	528	19.2	359	1	AG2R_MOUSE	TYPE-1A ANGIOTENSIN I	5.61e-79
42	528	19.2	359	1	AG2R_RAT	TYPE-1A ANGIOTENSIN I	5.61e-79
43	527	19.2	359	1	AG2S_MOUSE	TYPE-1B ANGIOTENSIN I	8.97e-79
44	523	19.1	359	1	AG2R_RABIT	TYPE-1 ANGIOTENSIN II	5.87e-78
45	523	19.1	363	1	AG2S_XENLA	TYPE-1-LIKE ANGIOTENS	5.87e-78

## ALIGNMENTS

RESULT	1	STANDARD;	PRT;	372 AA.
ID	OPRD_MOUSE			
AC	P32300;			
DT	01-OCT-1993 (REL. 27, CREATED)			
DT	01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	DELTA-TYPE OPIOID RECEPTOR (DOR-1) (K56) (MSL-2).			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 93101664.			
RA	KIEFFER B.L., BEFORT K., GAVERIAUX-RUFF C., HIRTH C.G.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 89:12048-12052(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 93110361.			
RA	EVANS C.J., KEITH D.E. JR., MORRISON H., MAGENDZO K., EDWARDS R.H.;			
RL	SCIENCE 258:1952-1955(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN;			
RX	MEDLINE; 93342064.			
RA	YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	KEITH D.E. JR., ANTON B., EVANS C.J.;			
RL	PROC. WEST. PHARMACOL. SOC. 36:299-306(1993).			
RN	[5]			
RP	SEQUENCE OF 8-372 FROM N.A.			
RX	MEDLINE; 94022364.			
RA	BZDEGA T., CHIN H., KIM K., JUNG H.H., KOZAK C.A., KLEE W.A.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 90:9305-9309(1993).			
RN	[6]			
RP	3D-STRUCTURE MODELLING.			
RX	MEDLINE; 97001837.			
RA	ALKORTA I., LOEW G.H.;			
RL	PROTEIN ENG. 9:573-583(1996).			
CC	-I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM			
CC	ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY			
CC	STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.			
CC	-I- TISSUE SPECIFICITY: BRAIN, WITH HIGH CONCENTRATIONS IN THE BASAL			
CC	GANGLIA AND LIMBIC REGIONS.			

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; L06322; G192943; -.  
DR EMBL; L07271; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; L11064; G348247; -.  
DR EMBL; S65335; G442326; -.  
DR EMBL; S66181; G435782; -.  
DR PIR; S37807; S37807.  
DR PIR; B48227; B48227.  
DR GCRDB; GCR\_0229; -.  
DR GCRDB; GCR\_0493; -.  
DR GCRDB; GCR\_0634; -.  
DR GCRDB; GCR\_0842; -.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR.  
DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).  
FT TRANSNM 46 75 1 (POTENTIAL).  
FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).  
FT TRANSNM 85 102 2 (POTENTIAL).  
FT DOMAIN 103 124 EXTRACELLULAR (POTENTIAL).  
FT TRANSNM 125 144 3 (POTENTIAL).  
FT DOMAIN 145 174 CYTOPLASMIC (POTENTIAL).  
FT TRANSNM 175 190 4 (POTENTIAL).  
FT DOMAIN 191 215 5 (POTENTIAL).  
FT TRANSNM 216 238 6 (POTENTIAL).  
FT DOMAIN 239 261 7 (POTENTIAL).  
FT TRANSNM 262 284 6 (POTENTIAL).  
FT DOMAIN 285 293 7 (POTENTIAL).  
FT TRANSNM 294 310 7 (POTENTIAL).  
FT DOMAIN 311 372 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 18 18 POTENTIAL.  
FT CARBOHYD 33 33 POTENTIAL.  
FT DISULFID 121 198 BY SIMILARITY.  
FT LIPID 333 333 PALMITATE (POTENTIAL).  
SQ SEQUENCE 372 AA; 40561 MW; 514022F5 CRC32;  
Query Match 100.0%; Score 2743; DB 7; Length 372;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 melypsaraelqssplvnlsda fspasaganasgspgarsasslalaialtalsavc 60  
QY 1 MELVPSARAELOSSPLVNLSDAFPSA FPSAGANASGSPGARSASSLALAIALTALSAYC 60  
Db 61 avglgnvnlvmfgivrytklktatniyifnlaladalatsltpfqsakylmetwpgell 120  
QY 61 AVGLGNVLVMFGIVRYTKLKTATNIYIFNLALADALATSTLPFQSAKYLMETWPGELL 120  
Db 121 ckavlsidyynmftsiflttmsvdyia vchpvykaldfrtpakakliniciwlasvgv 180  
QY 121 CKAVLSIDYYNMFSTIFLTLMMSVDRIYAVCHPYKALDFRTPAKAKLINICIWLASGVG 180  
Db 181 vplmwavtqprdgavvcmlqfppspwywdvtvkicvflfa fvpillitvcyglmllrl 240  
QY 181 VPIWMMAVTQPRDGA VVCM LQFPSPSWYWDVTVKICVFLFAFVVPILLITVCYGLMLLRL 240  
Db 241 rsvrllsgskekrslrrlrmvllvvga fvcwapihifviwtlvdinrdplvvaal 300  
QY 241 RSVRLLSGSKEKRS LRRITRMVLLVVGA FVVCWAPIHIFVIWTLVDINRDPLVVAAL 300  
Db 301 hlcialgyansslnpvlyafldenfkrcfrqlcrtpcgrqegpslrrprgattterrvtac 360  
QY 301 HLCIALGYANSS LNPVLYAFLDENFKRCFRQLCRTPCGRQEGPSLRRPRQATTREVRTAC 360  
Db 361 tpsdpgpgggaaa 372  
QY 361 TPSDGPGGGAAA 372  
RESULT 2 STANDARD; PRT; 372 AA.  
ID OPND\_RAT AC P33533;

DT 01-FEB-1994 (REL. 28, CREATED)  
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1) (OPIOID RECEPTOR A).  
GN ROR-A.  
OS RATTUS NORVEGICUS (RAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RX MEDLINE; 93351652.  
RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;  
RL FEBS LETT. 327:311-314(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;  
RX MEDLINE; 94322412.  
RA ABOOD M.E., NOEL M.A., FARNSWORTH J.S., TAO Q.;  
RL J. NEUROSCI. RES. 37:714-719(1994).  
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY  
CC STEREOSSELECTIVE. RECEPTOR FOR ENKEPHALINS.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; D16348; G391865; -.  
DR EMBL; U00475; G514211; -.  
DR PIR; S34592; S34592.  
DR GCRDB; GCR\_0638; -.  
DR GCRDB; GCR\_0805; -.  
DR GCRDB; GCR\_0805; -.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR.  
DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).  
FT TRANSNM 46 75 1 (POTENTIAL).  
FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).  
FT TRANSNM 85 102 2 (POTENTIAL).  
FT DOMAIN 103 124 3 (POTENTIAL).  
FT TRANSNM 125 144 4 (POTENTIAL).  
FT DOMAIN 145 174 4 (POTENTIAL).  
FT TRANSNM 175 190 4 (POTENTIAL).  
FT DOMAIN 191 215 5 (POTENTIAL).  
FT TRANSNM 216 238 5 (POTENTIAL).  
FT DOMAIN 239 261 6 (POTENTIAL).  
FT TRANSNM 262 284 6 (POTENTIAL).  
FT DOMAIN 285 293 6 (POTENTIAL).  
FT TRANSNM 294 310 7 (POTENTIAL).  
FT DOMAIN 311 372 7 (POTENTIAL).  
FT CARBOHYD 18 18 POTENTIAL.  
FT CARBOHYD 33 33 POTENTIAL.  
FT DISULFID 121 198 BY SIMILARITY.  
FT LIPID 333 333 PALMITATE (POTENTIAL).  
SQ SEQUENCE 372 AA; 40449 MW; 59F5EE50 CRC32;  
Query Match 96.9%; Score 2657; DB 7; Length 372;  
Best Local Similarity 97.0%; Pred. No. 0.00e+00;  
Matches 361; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
Db 1 meypsaraelqsilanvsdtfspa fspasaganasgspgarsasslalaialtalsavc 60  
QY 1 MELVPSARAELOSSPLVNLSDAFPSA FPSAGANASGSPGARSASSLALAIALTALSAYC 60  
Db 61 avglgnvnlvmfgivrytklktatniyifnlaladalatsltpfqsakylmetwpgell 120  
QY 61 AVGLGNVLVMFGIVRYTKLKTATNIYIFNLALADALATSTLPFQSAKYLMETWPGELL 120  
Db 121 ckavlsidyynmftsiflttmsvdyia vchpvykaldfrtpakakliniciwlasvgv 180  
QY 121 CKAVLSIDYYNMFSTIFLTLMMSVDRIYAVCHPYKALDFRTPAKAKLINICIWLASGVG 180  
Db 181 vplmwavtqprdgavvcmlqfppspwywdvtvkicvflfa fvpillitvcyglmllrl 240  
QY 181 VPIWMMAVTQPRDGA VVCM LQFPSPSWYWDVTVKICVFLFAFVVPILLITVCYGLMLLRL 240



Db 241 rsvrllsgskedrsllrrlrmvllvvvgafvvcwapihlfvltvldvldinrrdplvvaal 300  
QY 241 RSVRLLSGSKEDRSRLRRITRMVLLVVGAFVVCWAPIHIFVLTVLDVLDINRRDPLVVAAL 300  
Db 301 hlcialgyansslmpvlyafldenfkrcfrqlcrapcgqgpgslrrprgatarervtac 360  
QY 301 HLCIALGYANSSLMPLYAFLDENFKRCFRQLCRTPCGRQEPGSLRRPRQATTRERVTAAC 360  
Db 361 tpsdpgpggaaa 372  
QY 361 TPSDGPGGGAAA 372

RESULT 3  
ID OPRD\_HUMAN STANDARD; PRT: 372 AA.  
AC P41143;  
DT 01-FEB-1995 (REL. 31, CREATED)  
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
DE 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1).  
GN OPRD1 OR OPRD.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=CEREBRAL CORTEX, AND STRIATUM;  
RX MEDLINE: 94260835.  
RA KNAPP R.J., MALATYNSKA E., FANG L., LI X., BABIN E., NGUYEN M.,  
RA SANTORO G., VARGA E.V., HRUBY V.J., ROESKE W.R., YAMAMURA H.I.,  
RL LIFE SCI. 54:463-469(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 95107267.  
RA SIMONIN F., BEFORT K., GAVERIAUX-ROUF C., MATTHES H., NADDEY V.,  
RA IANNE B., MICHELETTI G., KIEFFER B.,  
RL MOL. PHARMACOL. 46:1015-1021(1994).  
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY  
STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL: U07882; G497314; -.  
DR EMBL: U10504; E162517; -.  
DR MIM: 165195; -.  
DR PROSITE: PS00237; G-PROTEIN\_RECEPTOR.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 46 75 1 (POTENTIAL).  
FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 85 102 2 (POTENTIAL).  
FT DOMAIN 103 124 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 125 144 3 (POTENTIAL).  
FT DOMAIN 145 174 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 175 190 4 (POTENTIAL).  
FT DOMAIN 191 215 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 216 238 5 (POTENTIAL).  
FT DOMAIN 239 261 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 262 284 6 (POTENTIAL).  
FT DOMAIN 285 293 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 294 310 7 (POTENTIAL).  
FT DOMAIN 311 372 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 18 18 POTENTIAL.  
FT CARBOHYD 33 33 BY SIMILARITY.  
FT DISULFID 121 198 PALMITATE (POTENTIAL).  
FT LIPID 333 333 F -> C (IN REF. 2).  
FT CONFLICT 27 27 PG -> AR (IN REF. 2).  
FT CONFLICT 40 41 F -> A (IN REF. 2).  
FT CONFLICT 348 348 P -> A (IN REF. 2).  
FT CONFLICT 370 370 R -> A (IN REF. 2).  
SQ SEQUENCE 372 AA; 40450 MW; CFF92985 CRC32;

Query Match 94.1%; Score 2581; DB 7; Length 372;  
Best Local Similarity 93.3%; Pred. No. 0.00e+00;  
Matches 347; Conservative 14; Mismatches 11; Indels 0; Gaps 0;  
Db 1 mepapsagaejqpplfnasdaypsafpsaganaagpppgsaslalalaysavc 60  
QY 1 MELVPSARAELOSSPLVNLSDAFPSAFPSAGANASGSPGARSASSIALAIALAYSAC 60  
Db 61 avglgnvlymfgivrytkmktatniyifnlaladalatslpfqsakylmetwfgell 120  
QY 61 AVGLGNVLYMFGIVRYTKLKTATNIYIFNLALADALATSLPFQSAKYLMETWRFCELL 120  
Db 121 ckavlsidymftsiftltmsvdyriavchpvcakldfrtpakakliniciwlasvg 180  
QY 121 CKAVLSIDYNNMFTSIFTLTMSVDYRIAVCHPVKALDFRTPAKAKLINICIWLASVGC 180  
Db 181 vpinwmaavlrrdgavvcmlqfppspwywdvtvkicvflfafvpillitvcyglmrl 240  
QY 181 VPIWMAAVLTQPRDGAVVCMQFPSPSWYWDVTVKICVFLEFAFVPIILITVCYGLMLRL 240  
Db 241 rsvrllsgskedrsllrrlrmvllvvvgafvvcwapihlfvltvldvldinrrdplvvaal 300  
QY 241 RSVRLLSGSKEDRSRLRRITRMVLLVVGAFVVCWAPIHIFVLTVLDVLDINRRDPLVVAAL 300  
Db 301 hlcialgyansslmpvlyafldenfkrcfrqlcrpgrdpssfsrpreatarervtac 360  
QY 301 HLCIALGYANSSLMPLYAFLDENFKRCFRQLCRTPCGRQEPGSLRRPRQATTRERVTAAC 360  
Db 361 tpsdpgpgggraa 372  
QY 361 TPSDGPGGGAAA 372

RESULT 4  
ID OPRD\_HUMAN STANDARD; PRT: 400 AA.  
AC P35372;  
DT 01-JUN-1994 (REL. 29, CREATED)  
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)  
DE 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
DE MU-TYPE OPIOID RECEPTOR (MOR-1).  
GN OPRM1 OR MOR1.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RX MEDLINE: 94139928.  
RA WANG J.-B., JOHNSON P.S., PERSICO A.M., HAWKINS A.L., GRIFFIN C.A.,  
RA UHL G.R.,  
RL FEBS LETT. 338:217-222(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RA MESTEK A. JR., HURLEY J.H., BYE L.S., CAMPBELL A., TIAN M.,  
RA CHEN Y., YU L.,  
RL SUBMITTED (XXX-1994) TO EMBL/GENBANK/DBJ DATA BANKS.  
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR  
FOR BETA-ENDOPHIN.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL: L25119; G452073; -.  
DR EMBL: L29301; G459832; -.  
DR GCRDB: GCR\_0885; -.  
DR GCRDB: GCR\_0966; -.  
DR MIM: 600018; -.  
DR PROSITE: PS00237; G-PROTEIN\_RECEPTOR.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 66 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 67 96 1 (POTENTIAL).

FT	DOMAIN	97	105	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	106	123	2 (POTENTIAL).
FT	DOMAIN	124	145	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	146	165	3 (POTENTIAL).
FT	DOMAIN	166	195	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	196	211	4 (POTENTIAL).
FT	DOMAIN	212	236	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	237	259	5 (POTENTIAL).
FT	DOMAIN	260	282	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	283	305	6 (POTENTIAL).
FT	DOMAIN	306	313	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	314	330	7 (POTENTIAL).
FT	DOMAIN	331	400	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	142	219	BY SIMILARITY.
FT	LIPID	353	353	PALMITATE (POTENTIAL).
FT	CARBOHYD	9	9	POTENTIAL.
FT	CARBOHYD	12	12	POTENTIAL.
FT	CARBOHYD	33	33	POTENTIAL.
FT	CARBOHYD	40	40	POTENTIAL.
FT	CARBOHYD	48	48	POTENTIAL.
FT	CONFLICT	51	51	N -> D (IN REF. 2).
FT	CONFLICT	234	234	V -> L (IN REF. 2).
SQ	SEQUENCE	400 AA;	44764 MW;	3F40D610 CRC32;

Query Match	Best Local Similarity	Matches	Score	Pred.	No.	DB	Length
220;	Conservative	63.0%;	1729;	0.00e+00;	58;	Mismatches	61;
						Indels	3;
						Gaps	3;

Db	40	nlscpcgnrtnlgrdslecppt-gspsmtaitimalysivcvgvlgfnlmylviry	98
QY	18	nlSDAFPSAFPSAGANASGSPGARSASLALAIATLALSACAVGLGNVLVMEGIYRY	77
Db	99	tkmktatniyifnlaladalatstlpfgsvnylmgtwptfgtlckivisidyyumftsif	158
QY	78	TKLKTATNTYTFNLALADALATSTLPFGSAKYLMTWPEGLLCKAVLSIDYNNMFTSIF	137
Db	159	tlctmsvdryiavchpykaldfrtpnakiinvonwlssaiglpvmfmatkkyrgsid	218
QY	138	TLTMSVDRYIAVCHPYKALDFRTPAKAKLINICLWLASGVGPIMVMAVTOQPRDGAUV	197
Db	219	ctltfshptwyenlvkicvfifafimpvliitvcyglmllrlksvrmllsgskekdnlr	278
QY	198	CMLQPPSPSWYMDVTAKICVFLFAFVVPILITTCYGLMLDLRLSVRLLSGSKEDRSIR	257
Db	279	ritrmvlvnavvifvcpibihyivikalvti-pettfgtvswhficialgytnsclnpyl	337
QY	258	RITRMVLVVGAFVVCWAPIHIFVIVWTLVDINRRDPLVVAALHLCIALGYANSLSNPYL	317
Db	338	yafidenfkrcfrefcjpssnieqnsustringt-rdhpst	378
QY	318	YAFIDENFKRCFRCQCRTPCGRQEPGSLRRPQATTRERYTA	359

RESULT	5	STANDARD;	PRT;	398 AA.
ID	OPRM_RAT			
AC	P33535;			
DE	01-FEB-1994 (REL. 28, CREATED)			
DT	01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)			
DT	01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)			
DE	MU-TYPE OPIOID RECEPTOR (MOR-1) (OPIOID RECEPTOR B) (MUOR1).			
GN	ROR-B.			
OS	RATUUS NORVEGICUS (RAT).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BRIN;			
RX	MEDLINE; 93351652.			
RA	FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;			
RL	FEBS LETT. 327:311-314(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BRIN;			

[illegible]

Db 110 laladalatstlpfgsvnylmgtpwfgtlckivisidyymftsiftlctmsvdrylav 169  
QY 91 laladalatstlpfQSAKYlMETWPEGELLCKAVLSIDYNNFTSIFTLTMSVDRYLA 150  
Db 170 chpvkaldfrtprnakivncwmlssaiglpvmfmattkkyrgsidctltfshptwyw 229  
QY 151 CHPVKALDFRTPAKAKLINICIMVLASGVGPIMVMAVYQPRDGA VCMLOFPSPSWYWD 210  
Db 230 nlkicvfifafimpvllitvcyglmllrlksvmlsgskednrlrritmvlvavf 289  
QY 211 TVTKICVFLFAFVVPILITVCYGLMLRLRSVRLISGSKEDRSLRRTRMVLYVGAF 270  
Db 290 lvcwtpihyvikaltl-pettftvswhfialgytnsclnpvlafidenfkrcfr 348  
QY 271 VVCWAPIHIEFVITWLVINDNRDPLVVAALHLCIALGYANSSINPVLAFIDENFKRCFR 330  
Db 349 efciptsstieqgnstirvqnt-rehps 376  
QY 331 QLCRTPCGRQEPGSLRRPRQATTREVRTA 359

RESULT 6  
ID OPRM\_MOUSE STANDARD; PRT; 398 AA.  
AC P42866;  
DT 01-NOV-1995 (REL. 32, CREATED)  
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
DE MU-TYPE OPIOID RECEPTOR (MOR-1).  
GN MOR.  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-C57BL/6; TISSUE=LIVER;  
RX MEDLINE; 94377496.  
RA MIN B.H., AUGUSTIN L.B., FELSHEIM R.F., FUCHS J.A., LOH H.H.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 91:9081-9085(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RX MEDLINE; 95377399.  
RA ROSSI G.C., PAN Y.X., BROWN G.P., PASTERNAK G.W.;  
RL FEBS LETT. 369:192-196(1995).  
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR  
FOR BETA-ENDOPHILIN.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; U10561; G565069; -.  
DR EMBL; U10558; G565069; JOINED.  
DR EMBL; U10559; G565069; JOINED.  
DR EMBL; U10560; G565069; JOINED.  
DR EMBL; U26915; G1055231; -.  
DR PROSITE; PS00237; G-PROTEIN\_RECEPTOR.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 64  
FT TRANSMEM 65 94  
FT DOMAIN 95 103  
FT TRANSMEM 104 121  
FT DOMAIN 122 143  
FT TRANSMEM 144 163  
FT DOMAIN 164 193  
FT TRANSMEM 194 209  
FT DOMAIN 210 234  
FT TRANSMEM 235 257  
FT DOMAIN 258 280  
FT TRANSMEM 281 303  
FT DOMAIN 304 311  
FT TRANSMEM 312 328  
FT DOMAIN 329 398  
EXTRACELLULAR (POTENTIAL).  
1 (POTENTIAL).  
CYTOPLASMIC (POTENTIAL).  
2 (POTENTIAL).  
EXTRACELLULAR (POTENTIAL).  
3 (POTENTIAL).  
CYTOPLASMIC (POTENTIAL).  
4 (POTENTIAL).  
EXTRACELLULAR (POTENTIAL).  
5 (POTENTIAL).  
CYTOPLASMIC (POTENTIAL).  
6 (POTENTIAL).  
EXTRACELLULAR (POTENTIAL).  
7 (POTENTIAL).  
CYTOPLASMIC (POTENTIAL).

FT DISULFID 140 217 BY SIMILARITY.  
FT LIPID 351 351 PALMITATE (POTENTIAL).  
FT CARBOHYD 9 9 POTENTIAL.  
FT CARBOHYD 31 31 POTENTIAL.  
FT CARBOHYD 38 38 POTENTIAL.  
FT CARBOHYD 46 46 POTENTIAL.  
SQ SEQUENCE 398 AA; 44421 MW; C0211489 CRC32;  
Query Match 62.6%; Score 1716; DB 7; Length 398;  
Best Local Similarity 66.7%; Pred. No. 0.00e+00;  
Matches 212; Conservative 55; Mismatches 49; Indels 2; Gaps 2;  
Db 61 gspsmvtaitalmalyisvcvvgifgnflvmyivrytkmktatniyifnaladalatst 120  
QY 42 SASSLALAIATAITADYSAYCAVGLGNVLVMEGIVRYTKKTATNTYIFNALADALATST 101  
Db 121 lpfgsvnylmgtpwfgnllckivisidyymftsiftlctmsvdrylavchpvkaldfrt 180  
QY 102 LPFQSAKYlMETWPEGELLCKAVLSIDYNNFTSIFTLTMSVDRYLA VCHPVKALDFRT 161  
Db 181 prnakivncwmlssaiglpvmfmattkkyrgsidctltfshptwywenllkicvfifa 240  
QY 162 PAKAKLINICIMVLASGVGPIMVMAVYQPRDGA VCMLOFPSPSWYWDVTYTKICVFLFA 221  
Db 241 fimpvllitvcyglmllrlksvmlsgskednrlrritmvlvavfivcwtphiy 300  
QY 222 FVVPILITVCYGLMLRLRSVRLISGSKEDRSLRRTRMVLYVGAFVVCWAPIHIEFV 281  
Db 301 likaltl-pettftvswhfialgytnsclnpvlafidenfkrcfrefciptsstie 359  
QY 282 lvtwlvindnrddplvvaalhlclalgyansslnpvlafidenfkrcfrolcrtpcgrqe 341  
Db 360 qgnsarirqnt-rehps 376  
QY 342 PGLRRPRQATTREVRTA 359

RESULT 7  
ID OPRM\_RAT STANDARD; PRT; 380 AA.  
AC P34975;  
DT 01-FEB-1994 (REL. 28, CREATED)  
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).  
GN KOR-D.  
OS RATTUS NORVEGICUS (RAI).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RX MEDLINE; 94059008.  
RA CHEN Y., MESTER A., LIU J., YU L.;  
RL BIOCHEM. J. 295:625-628(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 93374033.  
RA MINAMI M., TOYA T., KATAO Y., MAEKAWA K., NAKAMURA S., ONOGI T.,  
RA KANEKO S., SATOH M.;  
RL FEBS LETT. 329:291-295(1993).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;  
RX MEDLINE; 94059009.  
RA LI S., ZHU J., CHEN C., CHEN Y.-W., DERIEL J.K., ASHBY B.,  
RA LIU-CHEN L.-Y.;  
RL BIOCHEM. J. 295:629-633(1993).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;  
RX MEDLINE; 94052210.  
RA MENG F., XIE G.-X., THOMPSON R.C., MANSOUR A., GOLDSTEIN A.,  
RA WATSON S.J., AKIL H.;

RL PROC. NATL. ACAD. SCI. U.S.A. 90:9954-9958(1993).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WISTAR; TISSUE=BRAIN;  
RX MEDLINE; 93380575.  
RA NISHI M., TAKESHIMA H., FUKUDA K., KATO S., MORI K.;  
RL FEBS LETT. 330:77-80(1993).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY;  
RX MEDLINE; 95204422.  
RA YAKOVLEV A.G., KRUEGER K.E., FADEN A.I.;  
RL J. BIOL. CHEM. 270:6421-6424(1995).  
CC -I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR  
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF  
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.  
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; L22001; G409237; -.  
DR EMBL; D16829; G404116; -.  
DR EMBL; L22536; G425189; -.  
DR EMBL; U00442; G403487; -.  
DR EMBL; D16534; G415310; -.  
DR EMBL; U17995; G727260; -.  
DR EMBL; U17993; G727260; JOINED.  
DR EMBL; U17994; G727260; JOINED.  
DR PIR; S36143; S36143.  
DR PIR; S38825; S38825.  
DR GCRDB; GCR\_0636; -.  
DR GCRDB; GCR\_0724; -.  
DR GCRDB; GCR\_0790; -.  
DR GCRDB; GCR\_0804; -.  
DR GCRDB; GCR\_0804; -.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 59 85 1 (POTENTIAL).  
FT TRANSMEM 86 95 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 96 117 2 (POTENTIAL).  
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 133 154 3 (POTENTIAL).  
FT TRANSMEM 135 173 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 144 196 4 (POTENTIAL).  
FT TRANSMEM 147 196 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 197 222 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 223 247 5 (POTENTIAL).  
FT TRANSMEM 248 275 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 276 299 6 (POTENTIAL).  
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 312 333 7 (POTENTIAL).  
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 131 210 BY SIMILARITY.  
FT LIPID 345 345 PALMITATE (POTENTIAL).  
FT CARBOHYD 25 25 POTENTIAL.  
FT CARBOHYD 39 39 POTENTIAL.  
FT CONFLICT 42 42 V -> L (IN REF. 2).  
FT CONFLICT 345 345 C -> Y (IN REF. 3).  
SQ SEQUENCE 380 AA; 42688 MW; EE858A46 CRC32;  
Query Match 58.5%; Score 1604; DB 7; Length 380;  
Best Local Similarity 67.0%; Pred. No. 0.00e+00;  
Matches 207; Conservative 51; Mismatches 45; Indels 6; Gaps 5;

QY 167 LINICINVLASGVGPIMMAVTLQPRDGA-VV-CMLQFPSP--SWYWDVTYKICVFLFAF 222  
Db 236 vlpvllivcytllmlrlksvrlldsgsrekdnrlrrtkllyvvavfliwtpihlfl 295  
QY 223 vvpillitycylmllrlsvrllsgskdkdrlrrttrmvlvvgafvvcwapihifvi 282  
Db 296 vealgstshsta-vlssyyficialgytunslnpvyafldenfkrcfdicfpikmmer 354  
QY 283 vwtlvdinrkdplvvaalhcialgyanslnpvyafldenfkrqfrcpogroep 342  
Db 355 gslrrprqa 351  
QY 343 gslrrprqa 351  
RESULT 8  
ID OPRK HUMAN STANDARD; PRT; 380 AA.  
AC P41145;  
DT 01-FEB-1995 (REL. 31, CREATED)  
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).  
GN OPRK1 OR OPRK.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RX MEDLINE; 94338360.  
RA MANSOON E., BARE L.A., YANG D.;  
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:1431-1437(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RX MEDLINE; 95350200.  
RA SIMONIN F., GAVERIAUS-RUFF C., BEFORT K., LANNES B., MICHELETTI G.,  
RA MATTEI M.-G., CHARON G., BLOCH B., KIEFFER B.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 92:7006-7010(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE; 95174504.  
RA ZHU J., CHEN C., XUE J.C., KUNAPULI S., DERIEL J.K., LIU-CHEN L.-Y.;  
RL LIFE SCI. 56:201-207(1995).  
CC -I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR  
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF  
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.  
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; U11053; G532060; -.  
DR EMBL; U17298; G596070; -.  
DR EMBL; L37362; G722618; -.  
DR PIR; JC2338; JC2338.  
DR MIM; 165196; -.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 59 85 1 (POTENTIAL).  
FT TRANSMEM 86 95 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 96 117 2 (POTENTIAL).  
FT TRANSMEM 118 132 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 133 154 3 (POTENTIAL).  
FT TRANSMEM 135 173 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 174 196 4 (POTENTIAL).  
FT TRANSMEM 197 222 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 223 247 5 (POTENTIAL).  
FT TRANSMEM 248 275 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 276 299 6 (POTENTIAL).  
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 312 333 7 (POTENTIAL).





OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=HARTLEY; TISSUE=BRAIN;
RX	MEDLINE; 94224825.
RA	XIE G.X., MENG F., MANSOUR A., THOMPSON R.C., HOVERSTEN M.T.,
RA	GOLDSTEIN A., WATSON S.J., AKIL H.;
RL	PROC. NATL. ACAD. SCI. U.S.A. 91:3779-3783(1994).
CC	-I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC	ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC	FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
CC	AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR	EMBL; U04092; G476107; -.
DR	GCRDB; GCR_0991; -.
KW	PROSITE; PS00237; G_PROTEIN_RECEPTOR.
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW	PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT	DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 59 85 1 (POTENTIAL).
FT	DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 96 117 2 (POTENTIAL).
FT	DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 133 154 3 (POTENTIAL).
FT	DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 174 196 4 (POTENTIAL).
FT	DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 223 247 5 (POTENTIAL).
FT	DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 276 299 6 (POTENTIAL).
FT	DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 312 333 7 (POTENTIAL).
FT	DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
FT	DISULFID 131 210 BY SIMILARITY.
FT	LIPID 345 345 PALMITATE (POTENTIAL).
FT	CARBOHYD 25 25 POTENTIAL.
FT	CARBOHYD 39 39 POTENTIAL.
SO	SEQUENCE 380 AA; 42736 MW; F9F34C4C CRC32;

Query Match	58.0%;	Score 1592;	DB 7;	Length 380;
Best local similarity	64.9%;	Pred. No. 0.00e+00;		
Matches	200;	Conservative	55;	Mismatches 49; Indels 4; Gaps 4;
Db	57	alpvilataysvfvvlglvgnslvmfvilrlytkmktatniyifnlaladalvtltmpfgs	116	
QY	47	alalalatalysavcavgllgnvlvmfgrivrytklktatniyifnlaladalatltpfgs	106	
Db	117	tvylmswvpgdvlokiavisidyygmftsiftltmmsvdyriavchpvcakaldfrtplkak	176	
QY	107	akylmetwpegellckavlsidyymftsiftltmmsvdyriavchpvcakaldfrtptakak	166	
Db	177	liniciwlsssvgsaillgstkvrredvdiectsfgpdddysswdlfmkicvfvfafv	236	
QY	167	liniciwlasgvgvplmwavtqprdga-vv-cmlqfppspw-xwdtvtkicvflfaav	223	
Db	237	ipvliiivcytlmlrlkavrllsgsrekdnrlrtrlvvvavflicwtbphifilv	296	
QY	224	vpiliitvcyglmllrlrsvrrllsgskekdrrslrritrmvlvvgafvvcwapihifviv	283	
Db	297	ealgstshsta-alsyyfclalqytnssinplyafidenfkrcfrdfcpikmrmerq	355	
QY	284	wtlvdinrddplvvalhltclalgvansslnpvlyafldenfkrccfrcqlcrppcgroepg	343	
Db	356	stsvrvnt	363	
QY	344	slrrproa	351	
RESULT	11	STANDARD;	PRT;	370 AA.
ID	OPRX_HUMAN			
AC	P41146;			

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DT      01-FEB-1995 (REL. 31, CREATED)
DT      01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT      01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE      PROBABLE OPIOID RECEPTOR.

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OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.

RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN STEM;  
 RX MEDLINE; 94185768.  
 RA MOLLEREAU C., PARMENTIER M., MAILLEUX P., BUTOUR J.L., MOISAND C.,  
 RA CHALON P., CAPUT D., VASSART G., MEUNIER C.,  
 RL FEBS LETT. 341:33-38(1994).

RN [2]  
RP SEQUENCE FROM N.A.

RA LEE P.H., ZHU J., LIU-CHEN L., CHANG K.;  
SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

- FUNCTION: OPIOID RECEPTOR WITH A POTENTIAL ROLE IN MODULATING A

CC NUMBER OF BRAIN FUNCTIONS, INCLUDING INSULINOLIC BEHAVIORS AND  
CC EMOTIONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS  
CC WHICH INHIBITS ADENYLIC CYCLASE.

CC SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC  
CC  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC

DR	EMBL; X77130; G471317; -
DR	EMBL; U30185; G1144297; -

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DR      PIR; $43087; $43087.  
DR      GCRDB; GCR_0987; -.  
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DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;

NAME	LOCUS	ORGANISM	FUNCTION	REFERENCE
KW	1	50	PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.	
ET	DOMAIN		EXTRACELLULAR (POTENTIAL).	

FT	1	20	LAMINOCYTOGENESIS.
FT	51	77	1 (POTENTIAL).
FT	76	87	CYTODIASMIC (POTENTIAL).

FT	8 /	CITOPLASTIC (POTENTIAL).
DOMAIN	78	2 (POTENTIAL).
TRANSMEM	88	POTENTIAL.
ET	109	(POTENTIAL)

DOMAIN	110	124	EXTRACELLULAR (POTENTIAL).
ET	110		
ET	125	146	3 (POTENTIAL).
TRANSMEM	125		

FT	165	CYTOPLASMIC (POTENTIAL).
DOMAIN	147	
TRANSMEM	166	
EDM	188	4 (POTENTIAL).

TRANSMEM	100	EXTRACELLULAR (POTENTIAL).
FT	180	
FT	189	
DOMAIN	211	
	226	POTENTIAL)
	5	(POTENTIAL)

FT	TRANSMEM	212	236	3 (POTENTIAL).
FT	DOMAIN	237	264	CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	265	288	6 (POTENTIAL).
FT	DOMAIN	289	300	EXTRACELLULAR (POTENTIAL).

ITEM	322	7 (POTENTIAL).
TRANSMEM	301	
DOMAIN	323	
DOMAIN	370	
		CYTOPLASMIC (POTENTIAL).

[illegible]

FT	LIPID	334	PALMITATE (POLENIUM).
FT	CARBOHYD	21	POTENTIAL.

FT	28	POTENTIAL.
FT	39	POTENTIAL.
FT	39	POTENTIAL.

SEQUENCE 370 AA; 40693 MW; BE3C3E8F CRC32;

Query Match	Score	DB 7;	Length
53.68;	1471;		
56.38;			
	pred No. 1	63e-279;	

Best Local Similarity	56.3%;	Pred. NO. 1.03e 4/5/
Matches	180;	Conservative 66;
		Mismatches 72;
		Indel

Db 47 p1qlkvttivg1ylavcvg1lignclvmyvilrrhtkmktatniyifnlalala

045 SIATATAITATYSACVAGLLGNVLMEGIIVRYTKLTATNTIYFIENLALZ

43 SUBRAJALINGAM CAN COLLECT THE CASH FROM THE

[illegible]

QY 105 QSAKIMETWPFEGELLCKAVLSIDYYNMETSIFFLLIMMSVDRI IAVCHP

Db 167 agavnvalmalasvgypraimsgavedeeiclelveipptqdywgpvfi

QY 165 AKLINICIWYLASGVGVPIIMMAVTPQPRDGAIVVCMLOFPSPSWYWDVTYI

Db 227 pvlvlsvcyslmirrllrgvrlslgsrekdnrlrrlrlvlvwwavfygc

04 225 PIIITVCYIMLRLRSLRVLLSGSKKEDRLRITRMVLVVGAEVVC

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Db 287 g1-gvqpssetavallrfctalgynscnlpljyafldentkacfrkfcasallrrdgyv 345  
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Db 346 sdvr-siakdvalactse 364  
QY 345 LRRPRQATTRERVTACTPSD 364

RESULT 12  
ID OPX RAT STANDARD; PRI; 367 AA.  
AC P35370;  
DT 01-JUN-1994 (REL. 29, CREATED)  
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE PROBABLE OPIOID RECEPTOR (ROR-C) (XOR1).  
OS RAITUS NORVEGICUS (RAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WISTAR; TISSUE=BRAIN;  
RX MEDLINE; 94215703.  
RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H., IWABE N.,  
RA MIYATA T., HOUTANI T., SUGIMOTO T.;  
RL FEBS LETT. 343:42-46(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HIPPOCAMPUS;  
RA MENG F., XIE G., ALFRED M., THOMPSON R., HOVERSTEIN M., WATSON S.,  
RA AKIL H.;  
RL SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;  
RX MEDLINE; 94307401.  
RA BUNZOW J.R., SAEZ C., MORTRUD M., BOUVIER C., WILLIAMS J.T., LOW M.,  
RA GRANDY D.K.;  
RL FEBS LETT. 347:284-288(1994).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 94307400.  
RA CHEN Y., FAN Y., LIU J., MESTEK A., TIAN M., KOZAK C.A., YU L.;  
RL FEBS LETT. 347:279-283(1994).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE; 95096849.  
RA LACHOWICZ J.E., SHEN Y., MONSMA F.J., SIBLEY D.R.;  
RL J. NEUROCHEM. 64:34-40(1995).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE; 94298959.  
RA WANG J.B., JOHNSON P.S., IMAI Y., PERSICO A.M., OZENBERGER B.A.,  
RA EPPLER C.M., UHL G.R.;  
RL FEBS LETT. 348:75-79(1994).  
RN [7]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;  
RX MEDLINE; 95182817.  
RA WICK M.J., MINNERATH S.R., LIN X., ELDE R.P., LAW P.Y., LOH H.H.;  
RL BRAIN RES. MOL. BRAIN RES. 27:37-44(1994).  
CC -1- FUNCTION: OPIOID RECEPTOR WITH A POTENTIAL ROLE IN MODULATING A  
CC NUMBER OF BRAIN FUNCTIONS, INCLUDING INSTINCTIVE BEHAVIOURS AND  
CC EMOTIONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS  
CC WHICH INHIBITS ADENYLYL CYCLASE.  
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SEVERAL BRAIN AREAS.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; D16438; G53335; -.  
DR EMBL; U05239; G451844; -.

DR EMBL; U01913; G487965; -  
DR EMBL; L28144; G496220; -  
DR EMBL; U07871; G606803; -  
DR EMBL; L33916; G557200; -  
DR EMBL; L29419; G510719; -  
DR PIR; S46238; S46238.  
DR PIR; S43655; S43655.  
DR GCRDB; GCR\_0834; -  
DR GCRDB; GCR\_0898; -  
DR GCRDB; GCR\_0912; -  
DR PROSITE; PS00237; G-PROTEIN\_RECEPTOR.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 47  
FT TRANSMEM 48 74  
FT DOMAIN 75 84  
FT TRANSMEM 85 106  
FT DOMAIN 107 121  
FT TRANSMEM 122 143  
FT DOMAIN 144 162  
FT TRANSMEM 163 185  
FT DOMAIN 186 208  
FT TRANSMEM 209 233  
FT DOMAIN 234 261  
FT TRANSMEM 262 285  
FT DOMAIN 286 297  
FT TRANSMEM 298 319  
FT DOMAIN 320 365  
FT DISULFID 120 197  
Seq primer: -28M13 rev2 from Amersham  
High quality sequence stop: 262.

FEATURES  
source  
Location/Qualifiers  
1..338

/organism="Homo sapiens"  
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTACCAATCTGAAGTGGAGCGCGGCACATCTTTTCTTTTCTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by  
M.Fatima Bonaldo. This library was constructed from the  
same fetus as the fetal lung library, Soares fetal lung  
NbHL19W."

/clone="376118"  
/clone\_lib="Soares fetal heart NbHL19W"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
<1..>338

BASE COUNT 65 a 115 c 67 g 89 t 2 others  
ORIGIN

Query Match 28.7%; Score 326; DB 6; Length 338;  
Best local Similarity 98.2%; Pred. No. 0.00e+00;  
Matches 330; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 3 gggccctttcatctacgtctcttctacttcocgagtgcccttcatatggccanaat 62  
QY 384 GGCCCTTTCACTACCTGCTCTTACTTCCGAGTGCCCTTCACTATATGGCCACAAAT 443  
Db 63 atgacttaagctcagtcgcatcagtggtgcaacctgacctgcatctgtcactcatc 122  
QY 444 ATGACTTTAGCTCCAGTCGGCATACAGTGTGACACTCGCTGCATCTGTCACTCATTC 503  
Db 123 actaatcaagcgcctgctggaagcgtctctgtgcaaccgcttcccatggaactgc 182  
QY 504 ACTACATCAAGCGCCTGCTGTGAGACGCTCTTCTGTGACCGCTTCTCCCATGGCACTATGC 563  
Db 183 cttgcgcaacatcttcaagaactgcaactactactggggttcgcgccgtgatggcct 242

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QY      564 CTTGGCGCAACATCTTCAAGAACTGCACCTACTACTGGGGCTTCGCCGGCTGGATGGCCT 623
Db      243 attacatcaatcaaccctctctaacactccccctaacctacgagctcagcagtgaaactgg 302
QY      624 ATTACATCAATCAACCTCTCTACACTCCCCCTACTACGAGACTCAGCAGGTGAAGAACTGG 683
Db      303 cgcctcgcaatcttctgtatctcgnagctcggaact 338
QY      684 CGCTCGGCATCTTTGTGATCTGCCAGCTCGGCAACT 719

RESULT  14
ID      HSA40670 standard; RNA; EST; 338 BP.
AC      AA040670;
NI      g1516948
DT      31-AUG-1996 (Rel. 49, Created)
DE      31-AUG-1996 (Rel. 49, last updated, Version 1)
DE      z406808.r1 Soares fetal heart NbHHL19W Homo sapiens cDNA clone
DE      376118 5' similar to PIR:S52504 S52504 homolog of rat synaptic
DE      glycoprotein SC2 ;.
KW      EST.
OS      Homo sapiens (human)
OC      Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC      Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
RN      [1]
RP      1-338
RA      Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
RA      Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
RA      Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
RA      Trevasaki E., Waterston R., Williamson A., Wohlmann P., Wilson R.;
RA      "The WashU-Merck EST Project";
RL      Unpublished.
CC      Contact: Wilson RK WashU-Merck EST Project Washington University
CC      School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC      MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC      est@watson.wustl.edu This clone is available royalty-free through
CC      LIND; contact the IMAGE Consortium (info@image.lind.gov) for
CC      further information. Seq primer: -28M13 rev2 from Amersham High
CC      quality sequence stop: 262.
FH      Key Location/Qualifiers
FH      source 1..338
FH      /organism="Homo sapiens"
FH      /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
FH      modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
FH      strand cDNA was primed with a Not I - oligo(dT) primer [5',
FH      TGTACCAATCTGAAGTGGAGCGCGCCGATCTTTTCTTTTCTTTT 3'],
FH      TGTACCAATCTGAAGTGGAGCGCGCCGATCTTTTCTTTTCTTTT 3'],
FH      double-stranded cDNA was size selected, ligated to Eco RI
FH      adapters (Pharmacia), digested with Not I and cloned into
FH      the Not I and Eco RI sites of a modified pT7T3 vector
FH      (Pharmacia). Library went through one round of
FH      normalization to a Cot = 5. Library constructed by M.Fatim
FH      a
FT      Bernaldo. This library was constructed from the same fetus
FT      as the fetal lung library, Soares fetal lung NbHHL19W."
FT      /clone="376118"
FT      /clone_lib="Soares fetal heart NbHHL19W"
FT      /sex="unknown"
FT      /dev_stage="19 weeks"
FT      /lab_host="DH10B (ampicillin resistant)"
FT      <1..>338
FT      mRNA
FT      Sequence 338 BP; 65 A; 115 C; 67 G; 89 T; 2 other;
SQ

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Query Match 28.7%; Score 326; DB 229; Length 338;
Best Local Similarity 98.2%; Pred. No. 0.00e+00;
Matches 330; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db      3 gggccctttcatctacactgtctctctacttcgagtgcccttcacatcgtatggcacaat 62
QY      384 GGCCCTTTTCACTACCTGCTCTACTTCCGAGTGCCCTTCATCTATGGCCACAAT 443
Db      63 atgacttcaagtcagtcgcatcacagtggtgcacctcgctgcatctgtcaactatcc 122

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QY      444 ATGACTTACGTCCAGTCCGCAATACAGTGGTGACACCTCGCCCTGCATCTGTCACTCATTC 503
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QY      504 ACTACATCAAGCGCCTGCTGGAGACGCTCTTCTGTGACACCGCTTCTCCCATGGCACTATGC 563
Db      183 cttgcgcaacatcttcaagaactgcacctaactactggyggtctcgcgctggatggcct 242
QY      564 CTTGGCGCAACATCTTCAAGAACTGCACCTACTACTGGGGCTTCGCCGGCTGGATGGCCT 623
Db      243 attacatcaatcaaccctctctaacactccccctaacctacgagctcagcagtgaaactgg 302
QY      624 ATTACATCAATCAACCTCTCTACACTCCCCCTACTACGAGACTCAGCAGGTGAAGAACTGG 683
Db      303 cgcctcgcaatcttctgtatctcgnagctcggaact 338
QY      684 CGCTCGGCATCTTTGTGATCTGCCAGCTCGGCAACT 719

RESULT  15
LOCUS   R48780 387 bp mRNA EST 18-MAY-1995
DEFINITION Y169C08.s1 Homo sapiens cDNA clone 153998 3' similar to
SP:S5A2_HUMAN P31213 3-Oxo-5-ALPHA-STEROID 4-DEHYDROGENASE 2 ;.
ACCESSION R48780
NID      9810806
KEYWORDS EST.
SOURCE   human clone=153998 library=Soares breast 2NbHbst vector=pT7T3D
          (Pharmacia) with a modified polylinker host=DH10B (ampicillin
          resistant) primer=Promega -21m13 Rsite1=Not I Rsite2=Eco RI Adult
          female. 1st strand cDNA was primed with a Not I - oligo(dT) primer
          [5', TGTACCAATCTGAAGTGGAGCGCGCCGCTTTTCTTTTCTTTT 3'],
          [5', TGTACCAATCTGAAGTGGAGCGCGCCGCTTTTCTTTTCTTTT 3'],
          double-stranded cDNA was ligated to Eco RI adapters (Pharmacia),
          digested with Not I and cloned into the Not I and Eco RI sites of a
          modified pT7T3 vector (Pharmacia). Library went through one round
          of normalization to a Cot = 230. Library constructed by Bento
          Soares and M.Fatima Bernaldo.
          Homo sapiens
          Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
          Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
          Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;

ORGANISM XX
AC      xxxxxx
DT      01-JAN-1900
DE      Sequence 36, Application US/07769996C.
XX      Sequence 36, Application US/07769996C.
CC      GENERAL INFORMATION:
CC      APPLICANT: OKAYAMA, Hiroto
CC      APPLICANT: FUKE, Isao
CC      APPLICANT: MORI, Chisato
CC      APPLICANT: TAKAMIZAWA, Akahisa
CC      APPLICANT: YOSHIDA, Iwao
CC      TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
CC      TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
CC      NUMBER OF SEQUENCES: 50
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Armstrong, Westernman, Hattori, Mclelland
CC      ADDRESSSEE: & Naughton
CC      STREET: 1725 K St. N.W. Suite 1000
CC      CITY: Washington
CC      STATE: D.C.
CC      COUNTRY: U.S.A.
CC      ZIP: 20006
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/07/769,996C
CC      FILING DATE: 02-OCT-1991

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CC CLASSIFICATION: 424  
CC PRIOR APPLICATION DATA:  
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CC FILING DATE: 25-JUN-1990  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: JP 2-230921  
CC FILING DATE: 31-AUG-1990  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: JP 2-305605  
CC FILING DATE: 09-NOV-1990  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/635,451  
CC FILING DATE: 28-DEC-1990  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: McIeland, Le-Nhung  
CC REGISTRATION NUMBER: 31,541  
CC REFERENCE/DOCKET NUMBER: 900703B  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (202) 659-2930  
CC TELEFAX: (202) 887-0357  
CC TELEX: 440142  
CC INFORMATION FOR SEQ ID NO: 36:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 2621 amino acids  
CC TYPE: amino acid  
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CC MOLECULE TYPE: protein  
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QY 241 YMSKAHGIDPNIRITGRTITGAPVITYSTYGKFLADGGCGSGAYDIITICDECHSTDSTI 300  
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QY 301 LGIGTVLDQETAGARLVVLAATPPGSVTPHPNIEEVALSNTGEIPFYGAIPTEAIR 360  
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QY 361 GGRHLIFCHSKKKCDLAKLSGLGINAVAYYRGLDVSVIPTIGDVVVVATDALMTGYTG 420  
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QY 421 DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSGRRGTGRGRGIYRFVTPGE 480  
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QY 541 HIDAHLISQTKQAGDNFYLVAYOATVCARAQAPPSPWDQMWKCLIRLKPILHGPPTLLY 600

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Search completed: Fri Jul 18 08:22:46 1997  
Job time : 309 secs.

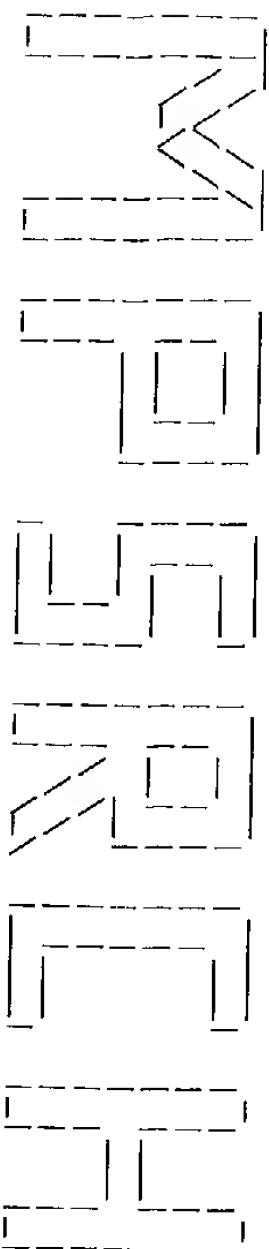
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FT CONFLICT 252 252 L -> V (IN REF. 1).  
SQ SEQUENCE 488 AA; 52920 MW; FE6A2C9F CRC32;

Query Match 19.9%; Score 79; DB 3; Length 488;  
Best Local Similarity 31.0%; Pred. No. 3.47e+00;  
Matches 13; Conservative 11; Mismatches 16; Indels 2; Gaps 2;

Db 92 walligigiatp-cvlpmyplisg-lylggkqrlstarall 131  
QY 3 WVLVGVLAALAAAYCLTTGSSVIVGRILISGRPAIVPDRELL 44

Search completed: Fri Jul 18 08:24:56 1997  
Job time : 22 secs.

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Aug 26 14:44:33 1997; MasPar time 10.17 Seconds

Tabular output not generated. 418.288 Million cell updates/sec

Title: >US-08-292-694A-4  
Description: (1-372) from US08292694A.pep  
Perfect Score: 2743  
Sequence: 1 MELVPSARAEIQSSPLVNL.....TRERVTACTPSDGGGAA 372

Scoring table: PAM 150  
Gap 11

Searched: 96640 seqs, 11439865 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq27  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20

Statistics: Mean 34.833; Variance 155.441; scale 0.224

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2743	100.0	372	13	R67670	Mouse delta opiod re	3.05e-247
2	2743	100.0	372	9	R48629	Sequence of murine de	3.05e-247
3	2650	96.6	372	14	R76782	Rat delta opiate rece	2.72e-238
4	2519	91.8	371	10	R66503	Murine delta opiod r	1.08e-225
5	1729	63.0	400	14	R76780	Human mu opiate recep	6.41e-150
6	1725	62.9	400	13	R71966	Human mu opiod recep	1.55e-149
7	1723	62.8	398	13	R71964	Rat mu opiod recep	2.40e-149
8	1721	62.7	356	11	R65188	Murine mu-subtype opi	3.73e-149
9	1721	62.7	398	14	R76781	Rat mu opiate recepto	3.73e-149
10	1604	58.5	380	14	R72591	Mammalian kappa opioi	5.63e-138
11	1604	58.5	380	14	R76783	Rat kappa opiate rece	5.63e-138
12	1604	58.5	380	17	R88722	Human kappa opiod re	5.63e-138
13	1597	58.2	380	13	R67669	Mouse kappa opiod re	2.62e-137
14	1463	53.3	367	13	R71968	Rat opiod receptor.	1.59e-124
15	1460	53.2	367	13	R67671	Mouse opiod receptor	3.07e-124
16	1455	53.0	295	12	R67672	Human kappa opiod re	9.20e-124
17	1454	53.0	367	14	R76638	Rat opiorph receptor	1.15e-123
18	1145	41.7	367	13	R74298	Mouse kappa-3 opiod	2.68e-94
19	957	34.9	391	7	R39259	Human somatostatin re	1.57e-76
20	957	34.9	391	7	R39260	Murine somatostatin r	1.57e-76

21	879	32.0	369	7	R39262	Murine somatostatin r	3.44e-69
22	873	31.8	333	13	R72985	Epsilon opiod recept	1.26e-68
23	871	31.8	369	19	R97269	Human somatostatin re	1.94e-68
24	871	31.8	369	7	R39261	Human somatostatin re	1.94e-68
25	869	31.7	369	5	R27504	Pituitary somatostati	3.00e-68
26	835	30.4	418	7	R39263	Human somatostatin re	4.66e-65
27	822	30.0	322	16	R48754	Rat RGH G-protein cou	7.71e-64
28	822	30.0	322	13	R72984	Rat RGH G-protein cou	7.71e-64
29	821	29.9	328	13	R39264	Epsilon opiod recept	9.57e-64
30	757	27.6	428	7	R39264	Murine somatostatin r	9.35e-58
31	605	22.1	349	14	R79443	Galanin receptor.	1.28e-43
32	603	22.0	349	18	R95070	Human galanin recepto	1.95e-43
33	578	21.1	402	18	R98358	Somatostatin-like rec	3.98e-41
34	569	20.7	355	11	R52749	C-C chemokine recepto	2.69e-40
35	563	20.5	348	17	R91229	Mouse pancreas G-prot	9.60e-40
36	563	20.5	348	18	R95069	Mouse pancreas beta-c	9.60e-40
37	514	18.7	355	18	W03378	CC-chemokine receptor	3.05e-35
38	511	18.6	325	15	R48730	G-protein coupled bov	5.74e-35
39	511	18.6	325	19	W02702	G-protein coupled bov	5.74e-35
40	505	18.4	355	20	W07618	Human G-protein recep	2.03e-34
41	497	18.1	380	10	R53750	Seven transmembrane r	1.10e-33
42	495	18.0	355	18	W03377	CC-chemokine receptor	1.67e-33
43	494	18.0	355	18	W03376	CC-chemokine receptor	2.06e-33
44	492	17.9	359	9	R44531	Human angiotensin II	3.14e-33
45	479	17.5	363	13	R66934	Mouse AT2 receptor.	4.83e-32

ALIGNMENTS

RESULT 1  
ID R67670 standard; Protein; 372 AA.  
AC R67670;  
DT 17-AUG-1995 (first entry)  
DE Mouse delta opiod receptor MOR1.  
KW Mouse; kappa; delta; mu; opiod receptor; brain; primer; PCR; amplify;  
KW transmembrane domain; somatostatin; receptor; human; expression vector;  
KW truncate; chimaeic; assay; probe.  
OS Mus musculus.  
PN W09428132-A.  
PD 08-DEC-1994.  
PF 20-MAY-1994; U05747.  
PR 20-MAY-1993; US-066296.  
PR 30-JUL-1993; US-100694.  
PR 05-NOV-1993; US-147592.  
PA (ARCH-) ARCH DEV CORP.  
PI Bell GI, Reisine T, Yasuda K;  
DR WPI; 95-022804/03.  
DR N-PSDB; Q75927  
PT Polynucleotides and peptides derived from opiod receptor  
PT polypeptides - for use in therapeutic compositions and in  
PT screening assays for useful drug substances.  
PS Claim 5; Page 215-221; 300pp; English.  
CC The amino acid sequence of the novel mouse delta opiod receptor MOR1.  
CC a fragment (amplified from the cDNA library with primers Q75929-30) as a  
CC probe. The primers are based on the conserved sequences present in the  
CC second and third transmembrane domains of somatostatin (SRIF) receptor  
CC subtypes SSTR1, SSTR2 and SSTR3. The 1.3 kb EcoRI-SacI fragment from the  
CC mouse delta opiod receptor clone, lambda msl-2, was subcloned into the  
CC CMV promoter-based expression vector pCMV-6c. The resultant construct  
CC pCMV-msl-2 was transfected into COS-1 cells for protein production. The  
CC gene encoding the opiod receptor can be used to produce complete, the  
CC truncated or chimaeic opiod receptor proteins. The opiod receptors  
CC thus produced are useful for the development of novel assays designed to  
CC select or improve substances, capable of interacting with the opiod  
CC receptor proteins, for use in diagnosis, drug design and therapeutic  
CC applications.  
SQ Sequence 372 AA;

Query Match 100.0%; Score 2743; DB 13; Length 372;  
Best Local Similarity 100.0%; Pred. No. 3.05e-247;  
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 melypsaraelqssplvnlsdafpsafpsaganasgspgarsasslalaialtalsavc 60
    |||||||
QY 1 MELVPSARAELQSSPLVNLSDAFPSAFPAGANASGSPGARSASSLALAIITALYSAVC 60
Db 61 avglgnvlyvmfgivrytklktatniyifnlaladalastlfpfsakylmetwpgell 120
    |||||||
QY 61 AVGLGNVLYVMFGIVRYTKLKTATNIYIFNLALADALATSTLFPQSAKYIMETWPGELL 120
Db 121 ckavlsidyymftsiftltmmsvdyiavchpvykaldfrtpakakliniciwlasgvg 180
    |||||||
QY 121 CKAVLSIDYYNMFTSIFLTMTMSVDRIYAVCHPVKALDFRTPAKAKLINICIWLASGVG 180
Db 181 vvimwavytqprdgavvcmlqfppspwywdvtvkicvflfafvwpililtvcyglmrl 240
    |||||||
QY 181 VPIMWAVTQPRDGAVVCMLQFPSPSWYWDVTVKICVFLFAFVWPILITVCYGLMLRL 240
Db 241 rsvrllsgskekdslrritrmvlyvvgafvvcwapihifivwlvldinrrdplvvaal 300
    |||||||
QY 241 RSVRLLSGSKEDSLRRITRMVLYVVGAFVVCWAPIHIFIVWLVLDINRRDPLVVAAL 300
Db 301 hlcialgyansslnpvlyafidenfkrcfqlcrtpcgrqepgsllrrpqatrrervtac 360
    |||||||
QY 301 HLCIALGYANSSLNPLYAFIDENFKRCFQLCRTCPCGRQEPGSLRRPQATTRERVTAAC 360
Db 361 tpsdpgpggaaa 372
    |||||||
QY 361 TPSDGPGGGAAA 372

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RESULT 2
ID R48629 standard; Protein; 372 AA.
AC R48629;
DT 15-SEP-1994 (first entry)
DE Sequence of murine delta opioid receptor deduced from the
DE DOR-1 cDNA clone.
KW Opioid receptor; morphine; opiate.
OS Mus musculus.
FH Key Location/Qualifiers
FT Region 46..75
FT /label= putative membrane spanning region
FT Region 85..102
FT /label= see above
FT Region 125..144
FT /label= see above
FT Region 168..189
FT /label= see above
FT Region 215..238
FT /label= see above
FT Region 262..284
FT /label= see above
FT Region 295..308
FT /label= see above
PN WO9404552-A.
PD 03-MAR-1994.
PR 13-ATG-1993; U07665.
PR 13-ATG-1992; US-929200.
PA (REGC ) UNIV CALIFORNIA.
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
DR WPI; 94-083099/10.
DR N-PSDB; Q56700.
PT DNA encoding opioid receptors and antibodies against this
PT receptor - used to express and locate these receptors, and screen
PT opds. for opioid (ant)agonist activity
PS Clain 10; Fig 5; 74pp; English.
CC A cDNA library was constructed using mRNA isolated from the NG109-15
CC cell line. A single clone, named the DOR-1 clone was isolated.
CC Comparisons with known sequences in GenBank showed highest homology
CC between DOR-1 and the G-protein-coupled somatostatin receptor. Other
CC features of the DOR-1 clone AA sequence deduced from the cDNA
CC sequence included 3 consensus glycosylation sites at residues 18 and
CC 33 (predicted to be in the extracellular N-terminal domain), and at
CC residue 310 (close to the C-terminus and predicted to be
CC intracellular). Phosphokinase C consensus sites are present within

```

CC predicted intracellular domains, at residues 242,255, 344 & 352.  
 CC Seven putative membrane-spanning regions were identified. The DOR-1  
 CC clone produces a delta receptor with a predicted mol. wt. of 40,558  
 CC kaltons prior to post-translational modifications.  
 SQ Sequence 372 AA;

Query Match 100.0%; Score 2743; DB 9; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 3.05e-247;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 melypsaraelqssplvnlsdafpsafpsaganasgspgarsasslalaialtalsavc 60
    |||||||
QY 1 MELVPSARAELQSSPLVNLSDAFPSAFPAGANASGSPGARSASSLALAIITALYSAVC 60
Db 61 avglgnvlyvmfgivrytklktatniyifnlaladalastlfpfsakylmetwpgell 120
    |||||||
QY 61 AVGLGNVLYVMFGIVRYTKLKTATNIYIFNLALADALATSTLFPQSAKYIMETWPGELL 120
Db 121 ckavlsidyymftsiftltmmsvdyiavchpvykaldfrtpakakliniciwlasgvg 180
    |||||||
QY 121 CKAVLSIDYYNMFTSIFLTMTMSVDRIYAVCHPVKALDFRTPAKAKLINICIWLASGVG 180
Db 181 vvimwavytqprdgavvcmlqfppspwywdvtvkicvflfafvwpililtvcyglmrl 240
    |||||||
QY 181 VPIMWAVTQPRDGAVVCMLQFPSPSWYWDVTVKICVFLFAFVWPILITVCYGLMLRL 240
Db 241 rsvrllsgskekdslrritrmvlyvvgafvvcwapihifivwlvldinrrdplvvaal 300
    |||||||
QY 241 RSVRLLSGSKEDSLRRITRMVLYVVGAFVVCWAPIHIFIVWLVLDINRRDPLVVAAL 300
Db 301 hlcialgyansslnpvlyafidenfkrcfqlcrtpcgrqepgsllrrpqatrrervtac 360
    |||||||
QY 301 HLCIALGYANSSLNPLYAFIDENFKRCFQLCRTCPCGRQEPGSLRRPQATTRERVTAAC 360
Db 361 tpsdpgpggaaa 372
    |||||||
QY 361 TPSDGPGGGAAA 372

```

```

RESULT 3
ID R76782 standard; Protein; 372 AA.
AC R76782;
DT 11-DEC-1995 (first entry)
DE Rat delta opiate receptor.
KW Delta opiate receptor; mu opiate receptor; hMOR; opiate agonist;
KW opiate antagonist; drug abuse; analgesic.
OS Rattus sp.
PN WO9520667-A1.
PD 03-AUG-1995.
PR 30-JAN-1995; U01144.
PR 28-JAN-1994; US-188275.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH ) US SEC DEPT HEALTH.
PI Johnson PS, Persico AM, Uhl G, Wang J;
DR WPI; 95-275452/36.
PT New DNA encoding human mu opiate receptor - used esp. for screening
PT opds. for activity as opiate agonists or antagonists
PS Disclosure; Page 28-29; 49pp; English.
CC hMOR cDNA was obtd. from a human cerebral cortical cDNA library
CC screened with fragments of a rat mu opiate receptor. The encoded
CC protein showed homology to rat mu, delta and kappa opiate
CC receptors (R76781-83).
CC Sequence 372 AA;
SQ

```

Query Match 96.6%; Score 2650; DB 14; Length 372;  
 Best Local Similarity 96.8%; Pred. No. 2.72e-238;  
 Matches 360; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

```

Db 1 meypsaraelqfslanvsdtfpaafpsasanasgspgarsasslalaialtalsavc 60
    |||||||
QY 1 MELVPSARAELQSSPLVNLSDAFPSAFPAGANASGSPGARSASSLALAIITALYSAVC 60
Db 61 avglgnvlyvmfgivrytklktatniyifnlaladalastlfpfsakylmetwpgell 120

```



QY	61	AVGLIGNVLMFGIVRYTKLKTATNITYIFENLALADALATSTLPFQSAKYMETWPFGEILL	120
Db	121	ckavlsidyymftsiftltmmsvdrayaovchpvkaldfrtpakaklnicivlasgyg	180
QY	121	CKAVLSIDYYNMFTSIFTLTMMASVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVG	180
Db	181	vplmwmavtqprdgavwctldqfspspwywdvtvkicvflfafvypallitvcyglmrlrl	240
QY	181	VPIMWMAVTQPRDGAVWCMLOFPSBSWYWDVTVKICVFLFAFVYVPLLITVCYGLMLRL	240
Db	241	rsvrllsgskekdrslrritrmvllvvvgafvvcwapihifvltwclvldinrrdplvvaal	300
QY	241	RSVRLLSGSKKEDRSLRRITRMVLLVVGAFVVCWAPIHIFVLTWCLVDINRRDPLVVAAL	300
Db	301	hicialgyansslnpvlyafldenfkrcfrqlcrapcgngbslrrprqatarervtac	360
QY	301	HUCIALGYANSSLNPVLYAFLDENFKRCFRQLCRTPCGRQBPGLRRPRQATTRERVTAC	360
Db	361	tpsdgpygggaaa 372	
QY	361	TPSDGPGGGAAA 372	

RESULT 4  
 ID R66503 standard; Protein; 371 AA.  
 AC R66503;  
 DT 19-JAN-1995 (first entry)  
 DE Murine delta opioid receptor.  
 KW delta opioid; enkephalin; receptor; mouse; murine; analgesic; pain;  
 KW drug addiction; neurological disorder; psychiatric; disorder;  
 KW cardiovascular disorder.  
 OS Mus musculus.  
 PN FR2697850-A.  
 PD 13-MAY-1994.  
 PF 10-NOV-1992; 013526.  
 PR 10-NOV-1992; FR-013526.  
 PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.  
 PI Kieffer B;  
 WP1; 94-178255/22.  
 DR N-PSDB; Q66656.  
 PT New nucleic acid encoding opioid receptor - and related  
 PT polypeptide, antisense nucleic acid, probes, recombinant cells  
 PT and ligands, useful in diagnosis and treatment of e.g.  
 PT neurological disorders  
 PS Claim 8; Page 19-20; 29pp; French.  
 CC A cDNA bank constructed from hybridoma NG108-15, was used to  
 CC transfect COS-1 cells. The cells were tested for ability to bind  
 CC tritium-labelled Tyr-D-Thr-Gly-Phe-Leu-Thr, in the presence or  
 CC absence of the opioid antagonist naloxone. Clone K56 was isolated  
 CC from a positive colony and found to contain a 2216bp insert. This  
 CC cDNA encodes a delta opioid (enkephalin) receptor with apparent  
 CC dissociation constant 1.4nM and Bmax 3.9-6.4 pmole/mg protein.  
 CC Sequence 371 AA;

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Query Match      91.8%; Score 2519; DB 10; Length 371;
Best Local Similarity 95.2%; Pred. No. 1.08e-225;
Matches 355; Conservative 0; Mismatches 15; Indels 3
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Db 1 melvpsaraelqssplvnlstdafpsafpsaganasgspgarsasslalaialaialysavc 60  
 QY 1 MELVPSARAELQSSPLVNLSDAFPSAFPSPAGANASGSPGARSASSLALAIALAIALYSAVC 60  
 Db 61 avglldgvlvmfqivrytcklktatniyifnlaladalatslpfqsakylmetwpgell 120  
 QY 61 AVGLLDGNVLVMEFQIVRYTKLKTATNIYIFNLALADALATSTLPFQSAKYLMEWTWPGELL 120  
 Db 121 ckavlsidymfstsiftltmsvdryiavchpvcakldfrtpakaklinciwlasgyg 180  
 QY 121 CKAVLSIDYMKFTSIFTLTMSVDRIAVCHPVCALDERTPAKAKLINCIWVLASGYG 180  
 Db 181 vpinmwavtppgmwqwyacs-sspvql-vldtvcikicvflfafvvpilittvcyglmllr 238  
 QY 181 VPINMWAVTPPGMWQWYACS-SSPVQL-VLDTVCIKICVFLFAFVVPILITTCYGLMILLR 238

QY	181	VPIIMAVATQPRDGA-VVCMLOPPSPSWTMDTVTKICVFLFAFVVPILITVCTGLMLLR	239
Db	239	lrsvlllsgskskedrsllrrltmvlvvvgafvvcwapihifvltwltvdinrrdplvaa	298
QY	240	lrsvlllsgskskedrsllrrltmvlvvvgafvvcwapihifvltwltvdinrrdplvaa	299
Db	299	lhlcialgyansslnpvlyafldenfkrcfrqlcrtpcgrqepgsllrprqatrrervta	358
QY	300	lhlcialgyansslnpvlyafldenfkrcfrqlcrtpcgrqepgsllrprqatrrervta	359
Db	359	ctpsdgpypgggaaa	371
QY	360	ctpsdgpypgggaaa	372

	RESULT	5
ID	R76780	standard; Protein; 400 AA.
AC	R76780;	
DT	11-DEC-1995	(first entry)
DE	Human mu opiate receptor.	
KW	Mu opiate receptor; hMOR;	opiate agonist; opiate antagonist;
KW	drug abuse; analgesic.	
OS	Homo sapiens.	

FH	Key	Location/Qualifiers
FT	Modified_site	9
FT	/label= Glycosylation	
FT	/note= "N-linked glycosylation site"	
FT	Modified_site	11
FT	/label= Glycosylation	
FT	/note= "N-linked glycosylation site"	
FT	Modified_site	32
FT	/label= Glycosylation	
FT	/note= "N-linked glycosylation site"	
FT	Modified_site	40
FT	/label= Glycosylation	
FT	/note= "N-linked glycosylation site"	
FT	Modified_site	48
FT	/label= Glycosylation	
FT	/note= "N-linked glycosylation"	
FT	Domain	68..87
FT	/label= Transmembrane_domain	
FT	Domain	107..125
FT	/label= Transmembrane_domain	
FT	Domain	144..165
FT	/label= Transmembrane_domain	
FT	Domain	188..208
FT	/label= Transmembrane_domain	
FT	Domain	236..256
FT	/label= Transmembrane_domain	
FT	Domain	284..304
FT	/label= Transmembrane_domain	
FT	Domain	322..341
PN	/label= Transmembrane_domain	
PD	W09520667-A1.	
PD	03-AUG-1995.	
PF	30-JAN-1995; U01144.	
PR	28-JAN-1994; US-188275.	
PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.	
PI	(USSH ) US SEC DEPT HEALTH.	
DR	Johnson PS, Persico AM, Uhl G, Wang J;	
DR	WTI; 95-275452/36.	
DR	N-Psdb; Q93102.	
PT	New DNA encoding human mu opiate receptor - used esp. for screening	
PT	cpds. for activity as opiate agonists or antagonists	
PS	Claim 1; Page 25-26; 49pp; English.	
CC	hmOR cDNA was obtd. from a human cerebral cortical cDNA library	
CC	screened with fragments of a rat mu opiate receptor. Expression	
CC	of hmORI in COS cells revealed high affinity recognition of the mu	
CC	opiate specific ligand. Recombinant hmORI can be used to screen	
CC	compounds for analgesic activity.	
SQ	Sequence 400 AA;	

Query Match	Score	DB	Length
63.08;	1729;	14;	400;

	Best Local Similarity	64.3%;	Pred. NO. 6,41e-150;	
	Matches	220;	Conservative	58; Mismatches 61; Indels 3; Gaps 3;
Db	40	nlsdpcpnrtnlgyrdslopt-gspsmितातimalysivcvgylfgnflwmyivry	98	
QY	18	nlsdAFPSAFPSAGANASGSPGARSASSLALAIATIALYSACVAGLLGNVLVMFGIVRY	77	
Db	99	tkmktatniyifnlaladalatatstlpfgsvnylmgtwpfgrllckivisidymnftsif	158	
QY	78	TKIKTATNIYIENLALDALATSTLFPQSAKYIMETWPFGEILLCKAVLSIDYNNMFTSIF	137	
Db	159	tlctmsvdryiaevchpkyaldfrtrpnaklinvcawilssaiqlpvmfmattkkyrggsid	218	
QY	138	TLTMSVSDRYIAVCHPXYALDFRTPAKAKLINICIWLASGVPIIMMAVTQPRDGAVV	197	
Db	219	ctltfshptwyenlvykicvffafafimpvllltvcyglmllrksvrmlsgskekdnlr	278	
QY	198	CMLQFPSPSWMYMDVTATKICVFLEFAFVVPILLITVCYGLMLRLRSRYKLLSGSKEKDRSLR	257	
Db	279	ritrmvllvvavfivcwtbplhiyvilikalvti-pettfgtqswnfciatlgytusclnpvl	337	
QY	258	RITRMVLLVVGAFFVVCWAPIHIEFVIVTWLLVDINRRDPLVVAALHLCTALGYANSSLNPLV	317	
Db	338	yafldenfkrcfrefcipcitsniequnstrirgnt-rdhpst	378	
QY	318	YAFLDENFKRCFRCQLCRTPCGRQEPGSLRRPRQATIRERVTA	359	

RESULT 6  
ID R71966 standard; Protein; 400 AA.  
AC R71966;  
DT 20-OCT-1995 (first entry)  
DE Human mu opioid receptor.  
KW Mu opioid receptor; MOR; gene therapy; diagnostic.  
OS Homo sapiens.  
PN W09507983-A.  
PD 23-MAR-1995.  
PF 13-SEP-1994; U10358.  
PR 13-SEP-1993; US-120601.  
PA (INDV ) UNIV INDIANA FOUND.  
PI Yu L;  
DR WPI: 95-131351/17.  
DR N-PSDB; Q89226.  
PT New nucleic acid encoding new human mu opioid receptor - and  
PT related vectors, transformed cells, antibodies etc., useful in  
PT diagnosis, treatment and drug screening.  
PS Claim 4; Page 211-214; 266pp; English.  
CC A cDNA library constructed from human caudate nucleus mRNA was  
CC screened with rat mu opioid receptor cDNA under conditions of  
CC low stringency. One positive clone included the sequence given in  
CC Q89226, encoding a mu opioid receptor MOR (R71964). The cDNA  
CC is used for prodn. of recombinant MOR, in gene therapy, etc.  
SQ Sequence 400 AA;

Query Match	62.9%;	Score 1725;	DB 13;	Length 400;
Best Local Similarity	64.3%;	Pred. No. 1.55e-149;		
Matches 220;	Conservative	57;	Mismatches 62;	Indels 3;
				Gaps 3;

Db	40	nlsdpcgnrtldlggrdslocpt-gspsmaitaimalysivcvgqlfgnflvmvlyvry	98
		: :   : : :   :           :	
QY	18	NLSDAFSPSAFPSAGANASGSPGARSSASTLALAITALYSACVAGVLLGNVLVMEGIVRY	77
Db	99	tkmktatniyifnaladalatstlpfgsvnylmgtwpfgtilckivisidyyumftsif	158
QY	78	TKLKTATNIYIFNLALADALATSTLPFGSAKYLMEWMPFEGELCKAVLSIDYYNMFTSIF	137
Db	159	tletmsvdryiaevhpbvkaldfrtprnaklinvcwmlssaisglpvmfmatckyzgsid	218
QY	138	TLTMSVDRIYIACHPEPKALDFRTPAKAKLINICINVLASGVGPIMVMAYTQPRDGAVV	197
Db	219	ctltfshptwyenllkicvffafafimpvllitvcyglmllrlksvrmlsgskekdnr	278
QY	198	CMLQFPSPSPWMDVTYKICVLELLFAFVVPILITTCYGLMLLRSLRSVRLLSGSKKEKDRSLR	257

[illegible]

RESULT 7  
 ID R71964 standard; Protein; 398 AA.  
 AC R71964;  
 DT 20-OCT-1995 (first entry)  
 DE Rat mu opioid receptor.  
 KW Mu opioid receptor; MOR-1; gene therapy; diagnostic.  
 OS Rattus sp.  
 PN W09507983-A.  
 PD 23-MAR-1995.  
 PE 13-SEP-1994; U10358.  
 PR 13-SEP-1993; US-120601.  
 PA (INDV ) UNIV INDIANA FOUND.  
 PI Yu L;  
 DR WPI; 95-131351/17.  
 DR N-PSDB; Q89222.  
 PT New nucleic acid encoding new human mu opioid receptor - and  
 PT related vectors, transformed cells, antibodies etc., useful in  
 PT diagnosis, treatment and drug screening.  
 PS Disclosure; Page 190-194; 266pp; English.  
 CC A 365 bp fragment of the mouse delta opioid receptor was used to  
 CC screen a rat brain cDNA library under low stringency conditions.  
 CC One positive clone included the sequence given in Q89222, encoding a  
 CC mu opioid receptor, MOR-1 (R71964). MOR-1 was stably expressed in  
 CC transfected CHO cells.  
 CC Sequence 398 AA;  
 SQ

Query Match	62.8%;	Score 1723;	DB 13;	Length 398;
Best Local Similarity	66.0%;	Pred. No. 2,40e-149;		
Matches 217;	Conservative	55;	Mismatches 54;	Indels 3;
				Gaps 3;

D	51	gndslcpqr-gspsmvtaitymalysivcvgvlgfnflvmvivrvtckmktatniyifn	109
Q	31	GANASGSPGARSSALALAIATAITALYSAVCAVGLLGNVLVMEFIVRYTKTKATNIIYFN	90
D	110	laladalatstlprfqsvnylmgtwpfgtllckivisidyymftsiftlctmsvdryia	169
Q	91	LALADALATSTLPRFQSAKYMETWPFGEILCKRAVLSIDYNNMFTSIFTLLNMSVDRIYAV	150
D	170	chpykaldfrtprnakivncvnilssaiqlpvmfmattkkyrgsidctltfshptwywe	229
Q	151	CHPYKALDERTPAKAKLINICIWVLASGVGPIMYAAVTPQPRDGAVVCMLOFSPSWYWD	210
D	230	nllkicvlfafimpililtvcyglmllrkisvrmsgskekdnllritrmvllvvaaf	289
Q	211	TVTRKICVLEFAFVVPILITVCYGLMLLRLSVRLLSGSKEKDRSLRRITRMVLLVVGAF	270
D	290	ivcwtpihilyvlikaltili-pettfgtvswhfciaiqytnscinpviyaflidenfkrcfr	348
Q	271	VYCWAPIHIFVIWTLVDINRRDPLVVAALHLCIALGYANSSLNPLVYAFLEDENPKRCFR	330
D	349	efciaptsltieqgnstrvrqnt-rehps	376
Q	331	QLCRLPCGRQEPGSLRRPRQATTRREYTA	359

RESULT	8	
ID	R65188	standard; Protein; 356 AA.
AC	R65188.	
DT	19-APR-1995	(first entry)
DE	Murine mu-subtype opioid receptor.	
KW	Mu-subtype opioid receptor; MSOR; drug addiction.	
OS	Rattus rattus.	
FN	Key	Location/Qualifiers

FT Modified\_site 10..12  
FT /note= "Putative N-linked glycosylation site"  
FT Modified\_site 230  
FT /note= "Threonine residue especially favourable  
FT for protein kinase A phosphorylation"  
FT Region 25..48  
FT /note= "hydrophobic membrane spanning region"  
FT Region 58..78  
FT /note= "hydrophobic membrane spanning region"  
FT Region 96..118  
FT /note= "hydrophobic membrane spanning region"  
FT Region 139..166  
FT /note= "hydrophobic membrane spanning region"  
FT Region 187..212  
FT /note= "hydrophobic membrane spanning region"  
FT Region 236..257  
FT /note= "hydrophobic membrane spanning region"  
FT Region 274..294  
FT /note= "hydrophobic membrane spanning region"  
PN EP-612845-A.  
PD 31-AUG-1994.  
PF 09-FEB-1994; 101968.  
PR 26-FEB-1993; US-026140.  
PA (AMCT ) AMERICAN CYANAMID CO.  
PI Corbett MJ, Eppler CM, Shieh H, Zysk JR;  
DR WPI; 94-265963/33.  
DR N-PSDB; Q79199.  
PT Pure mu-type opioid receptor protein - and nucleic acid coding  
PT for it  
PS Claim 2; Fig 9; 39pp; English.  
CC R65188 is the rat mu-subtype opioid receptor protein purified  
CC from rat brain membranes, with biotinyl-b-endorphin (R56666)  
CC as its ligand. It is encoded by the nucleotide sequence Q79199  
CC which was synthesised using Q71022 and Q71023 as PCR primers.  
CC R65188 is useful for identifying othe receptor subtypes, for  
CC screening new opioid ligands, and for studying mechanisms of  
CC opioid action, e.g. drug addiction.  
SQ Sequence 356 AA;

Query Match 62.7%; Score 1721; DB 11; Length 356;  
Best Local Similarity 65.7%; Pred. No. 3.73e-149;  
Matches 216; Conservative 56; Mismatches 54; Indels 3; Gaps 3;  
Db 9 gnds1cpqt-gpsmvta1timalysivcvg1fgnflvmviviyrktmktatniyifn 67  
QY 31 GANASGSPGARSSALALAIATLALYSAYCAVGLGNVLMFGIVRYTKLTATNIYIFN 90  
Db 68 laladalatstlpfgsvnylmgtpfgtllckivisidyymftsiflctmsvdyriav 127  
QY 91 LALADALATSTLPFGSAKYLMETWPFGEILLCKAVLSIDYYNMFSTIFLLTMSVDRIYAV 150  
Db 128 chpvkaldfrtprnakivncvwlssaiglpvmfmatckyrqgsidctltfshptwyw 187  
QY 151 CHPVKALDFRTPAKAKLINICIMVLASGVGPIMVMAYVQPRDGAIVVCMLOFPSPSWYWD 210  
Db 188 nlkicvfi1afimpvllitvcyglmllrlksvmlsgskekdnlrritmvlvavf 247  
QY 211 TVTKICVFLFAFVVPILITVCGIMLLRLRSVRLLSGSKEDSLRITRMVLVVGAF 270  
Db 248 ivcwtpihyivlikaliti-pettfgtvswhfciatgynsclnplvlyafldenfkrcfr 306  
QY 271 VVCWAPIHIFIVITWTVLDINRDLVVAALHLCIALGYANSSINPVLVYAFIDENFKRCFR 330  
Db 307 efcipststieqgnstrvrgnt-rehps 334  
QY 331 QLCRTPCGRQEPGSLRRPRQATTRERVTA 359

RESULT 9  
ID R76781 standard; Protein; 398 AA.  
AC R76781;  
DT 11-DEC-1995 (first entry)  
DE Rat mu opiate receptor.

KW Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;  
KW drug abuse; analgesic.  
OS Rattus sp.  
PN WO9520667-A1.  
PD 03-AUG-1995.  
PE 30-JAN-1995; U01144.  
PR 28-JAN-1994; US-188275.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PI (USSH ) US SEC DEPT HEALTH.  
PI Johnson PS, Persico AM, Uhl G, Wang J;  
DR WPI; 95-275452/36.  
PT New DNA encoding human mu opiate receptor - used esp. for screening  
PT cpds. for activity as opiate agonists or antagonists  
PS Disclosure; Page 26-28; 49pp; English.  
CC hMOR cDNA was obtd. from a human cerebral cortical cDNA library  
CC screened with fragments of a rat mu opiate receptor. The encoded  
CC protein showed homology to rat mu, delta and kappa opiate  
CC receptors (R76781-83).  
SQ Sequence 398 AA;

Query Match 62.7%; Score 1721; DB 14; Length 398;  
Best Local Similarity 65.7%; Pred. No. 3.73e-149;  
Matches 216; Conservative 56; Mismatches 54; Indels 3; Gaps 3;  
Db 51 gnds1cpqt-gpsmvta1timalysivcvg1fgnflvmviviyrktmktatniyifn 109  
QY 31 GANASGSPGARSSALALAIATLALYSAYCAVGLGNVLMFGIVRYTKLTATNIYIFN 90  
Db 110 laladalatstlpfgsvnylmgtpfgtllckivisidyymftsiflctmsvdyriav 169  
QY 91 LALADALATSTLPFGSAKYLMETWPFGEILLCKAVLSIDYYNMFSTIFLLTMSVDRIYAV 150  
Db 170 chpvkaldfrtprnakivncvwlssaiglpvmfmatckyrqgsidctltfshptwyw 229  
QY 151 CHPVKALDFRTPAKAKLINICIMVLASGVGPIMVMAYVQPRDGAIVVCMLOFPSPSWYWD 210  
Db 230 nlkicvfi1afimpvllitvcyglmllrlksvmlsgskekdnlrritmvlvavf 289  
QY 211 TVTKICVFLFAFVVPILITVCGIMLLRLRSVRLLSGSKEDSLRITRMVLVVGAF 270  
Db 290 ivcwtpihyivlikaliti-pettfgtvswhfciatgynsclnplvlyafldenfkrcfr 348  
QY 271 VVCWAPIHIFIVITWTVLDINRDLVVAALHLCIALGYANSSINPVLVYAFIDENFKRCFR 330  
Db 349 efcipststieqgnstrvrgnt-rehps 376  
QY 331 QLCRTPCGRQEPGSLRRPRQATTRERVTA 359

RESULT 10  
ID R72591 standard; Protein; 380 AA.  
AC R72591;  
DT 01-DEC-1995 (first entry)  
DE Mammalian kappa opioid receptor protein.  
KW Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic;  
KW amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.  
OS Rattus rattus.  
FH Key Location/Qualifiers  
FT CDS 111..1253  
FT /tag= a  
FT /product= kappa opioid receptor  
PN J07070191-A.  
PD 14-MAR-1995.  
PE 30-JUL-1993; 190261.  
PR 09-JUL-1993; JP-170591.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
DR WPI; 95-144857/19.  
DR N-PSDB; Q86725.  
PT Kappa opioid receptor protein and cells expressing it - useful  
PT for the screening of compounds for analgesic and hypnotic  
PS properties  
PS Claim 2; Page 9-10; 15pp; Japanese.  
CC The amino acid sequence of the novel mammalian kappa opioid receptor.

CC The gene was isolated by amplifying a fragment from rat brain mRNA by  
CC reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from  
CC the mouse delta-opioid receptor gene. This fragment was cloned into the  
CC plasmid pCRIT to produce pRIT. The plasmid pRIT was used to probe a rat  
CC brain DNA library in lambda ZAP1 to obtain a clone of the rat kappa  
CC opioid receptor gene, designated pKOPR2. This clone was introduced into  
CC E.coli JM109 for production of the receptor protein. The receptor protein  
CC is useful for screening of analgesic and hypnotic compounds including  
CC peptides and proteins.  
SQ Sequence 380 AA;

Query Match 58.5%; Score 1604; DB 14; Length 380;  
Best Local Similarity 67.0%; Pred. No. 5.63e-138;  
Matches 207; Conservative 51; Mismatches 45; Indels 6; Gaps 5;

Db 57 aipvilitavysvfvvglvgnslvmfvilrvtkmktatniylfnaladalvttmpfqs 116  
|:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |:::|||||  
QY 47 ALAIALTAIXSAVCAGVGLGNVLVMEGIVRYTKLTATNTYIFNLADALATSTLPFQS 106  
Db 117 evylnmswpgfdvlgckivisiidymnftsiftlmsvdryiavchpvkaldfrtpk 176  
|:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |:::|||||  
QY 107 AKYIMETWPFGEELCKAVLSIDYNNFTSIFLTMMMSVDRIYAVCHPVKALDFRTPAKAK 166  
Db 177 liniciwllassvgisaivlggtkvrredvdlscslqfpddeysw-wdlfmkicvfvfaf 235  
|:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |:::|||||  
QY 167 LINICIWVLASGVGPIMWMAVTQPRDGA-VV-CMLQFPSP--SWYWDVTWKICVFLFAF 222  
Db 236 vipvllitvcytlmlrlksvrlslgsrekdrnlrritklvlvavavfiicwtpihifil 295  
|:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |:::|||||  
QY 223 VVPILITVCYGLMLRLRSVRLSLGSKKDRSLRRTRMVLVVGAFVVCWAPIHIFVI 282  
Db 296 vealgstshsta-vlssyyficialgytnslnpvlyafldenfkrcfrdcfipikmmer 354  
|:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |:::|||||  
QY 283 VMTLVDIRRDPDLVVAALHICIALGYANSSLPVLYAFLDENFKRCFRQLCRTPCGRQEP 342  
Db 355 qstnrvt 363  
|:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |:::|||||  
QY 343 GSLRRPRQA 351

RESULT 11  
ID R76783 standard; Protein; 380 AA.  
AC R76783;  
DI 11-DEC-1995 (first entry)  
DE Rat kappa opiate receptor.  
KW Kappa opiate receptor; mu opiate receptor; hMOR; opiate agonist;  
KW opiate antagonist; drug abuse; analgesic.  
OS Rattus sp.  
PN WO9520667-A1.  
PD 03-AUG-1995.  
PF 30-JAN-1995; U01144.  
PR 28-JAN-1994; US-188275.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PI (USSH ) US SEC DEPT HEALTH.  
PI Johnson PS, Persico AM, Uhl G, Wang J;  
WPI; 95-275452/36.  
DR New DNA encoding human mu opiate receptor - used esp. for screening  
PT cpgs. for activity as opiate agonists or antagonists  
PS Disclosure; Page 29-30; 49pp; English.  
CC hMOR cDNA was obt'd. from a human cerebral cortical cDNA library  
CC screened with fragments of a rat mu opiate receptor. The encoded  
CC protein showed homology to rat mu, delta and kappa opiate  
CC receptors (R76781-83).  
CC CC  
SQ Sequence 380 AA;

Query Match 58.5%; Score 1604; DB 14; Length 380;  
Best Local Similarity 67.0%; Pred. No. 5.63e-138;  
Matches 207; Conservative 51; Mismatches 45; Indels 6; Gaps 5;

Db 57 aipvilitavysvfvvglvgnslvmfvilrvtkmktatniylfnaladalvttmpfqs 116  
|:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |:::|||||  
QY 47 ALAIALTAIXSAVCAGVGLGNVLVMEGIVRYTKLTATNTYIFNLADALATSTLPFQS 106

Db 117 avylnmswpgfdvlgckivisiidymnftsiftlmsvdryiavchpvkaldfrtpk 176  
|:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |:::|||||  
QY 107 AKYIMETWPFGEELCKAVLSIDYNNFTSIFLTMMMSVDRIYAVCHPVKALDFRTPAKAK 166  
Db 177 liniciwllassvgisaivlggtkvrredvdlscslqfpddeysw-wdlfmkicvfvfaf 235  
|:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |:::|||||  
QY 167 LINICIWVLASGVGPIMWMAVTQPRDGA-VV-CMLQFPSP--SWYWDVTWKICVFLFAF 222  
Db 236 vipvllitvcytlmlrlksvrlslgsrekdrnlrritklvlvavavfiicwtpihifil 295  
|:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |:::|||||  
QY 223 VVPILITVCYGLMLRLRSVRLSLGSKKDRSLRRTRMVLVVGAFVVCWAPIHIFVI 282  
Db 296 vealgstshsta-vlssyyficialgytnslnpvlyafldenfkrcfrdcfipikmmer 354  
|:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |:::|||||  
QY 283 VMTLVDIRRDPDLVVAALHICIALGYANSSLPVLYAFLDENFKRCFRQLCRTPCGRQEP 342  
Db 355 qstnrvt 363  
|:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |:::|||||  
QY 343 GSLRRPRQA 351

RESULT 12  
ID R88722 standard; Protein; 380 AA.  
AC R88722;  
DI 04-SEP-1996 (first entry)  
DE Human kappa opioid receptor.  
KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;  
KW neurology; diagnosis.  
OS Homo sapiens.  
PN WO9601898-A1.  
PD 25-JAN-1996.  
PF 07-JUL-1995; F00912.  
PR 11-JUL-1994; FR-008531.  
PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.  
PI Kieffer B, Simonin F;  
WPI; 96-097628/10.  
DR N-PSDB; T12530.  
PT New nucleic acid encoding the human Kappa opioid receptor - useful  
PT in diagnosis and therapy, and for isolating receptor ligands and  
PT modulators  
PS Claim 7; Page 13-15; 30pp; French.  
CC The sequence coding for the human kappa opioid receptor was  
CC obtained from two overlapping cDNA fragments isolated from a  
CC human placental cDNA library. The fragments were amplified from  
CC the library using PCR primers based on the sequence of human  
CC genomic clones which hybridised with a murine delta receptor cDNA  
CC probe. Nucleotide probes derived from the kappa opioid receptor  
CC coding sequence are useful for diagnosis of neurological, cardio-  
CC vascular and psychiatric disorders associated with opioid  
CC receptors. The receptor can be used for identifying e.g. agonists  
CC of its activity for potential use as analgesics.  
CC CC  
SQ Sequence 380 AA;

Query Match 58.5%; Score 1604; DB 17; Length 380;  
Best Local Similarity 63.6%; Pred. No. 5.63e-138;  
Matches 213; Conservative 56; Mismatches 59; Indels 7; Gaps 7;

Db 30 fpywaepdngsagsedaqlcpahispalpilitavysvfvvglvgnslvmfvilrvtk 89  
|:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |:::|||||  
QY 23 FPS-AFP-SAGANASGSPGARSAS-SLALAIALTAIXSAVCAGVGLGNVLVMEGIVRYTK 79  
Db 90 mktatniylfnaladalvttmpfqsstvlmmswpgfdvlgckivisiidymnftsiftl 149  
|:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |:::|||||  
QY 80 LKTAATNIXIFNLALADALATSTLPFQSAKYIMETWPFGEELCKAVLSIDYNNFTSIFTL 139  
Db 150 tmmesvdyriavchpvkaldfrtpkakiniciwllssvgisaivlggtkvrredvle 209  
|:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |:::|||||  
QY 140 TMMMSVDRIYAVCHPVKALDFRTPAKAKLINICIWVLASGVGPIMWMAVTQPRDGA-VV- 197  
Db 210 csllqfpddyswdlfmkicvfiifvlpvllivcytlmlrlksvrlslgsrekdrnl 269  
|:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |:::|||||  
QY 198 CMLQFPSPSW-YMDVTWKICVFLFAFVVPILITVCYGLMLRLRSVRLSLGSKKDRSL 256



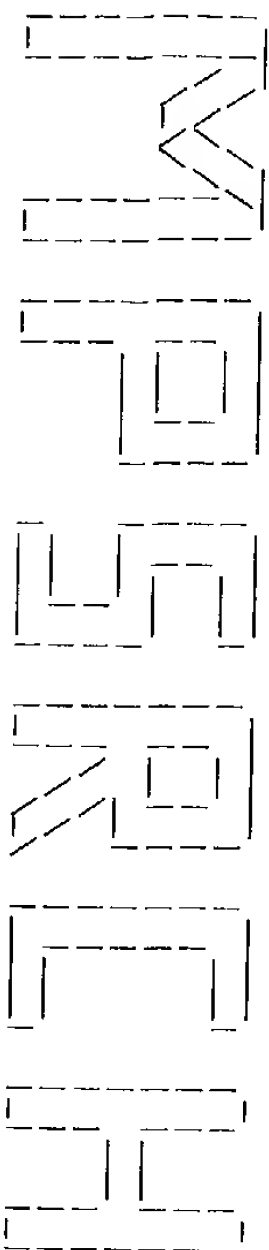


ER 20-MAY-1993; US-066296.  
 PR 30-JUL-1993; US-100694.  
 PR 05-NOV-1993; US-147592.  
 PA (ARCH-) ARCH DEV CORP.  
 PI Bell GI, Reisine T, Yasuda K;  
 DR WPI; 95-022804/03.  
 DR N-PSDE; Q75928.  
 PT polynucleotides and peptides derived from opioid receptor  
 PT polypeptides - for use in therapeutic compositions and in  
 PT screening assays for useful drug substances.  
 PS Claim 27; Page 225-229; 300pp; English.  
 CC The amino acid sequence of the novel mouse opioid receptor-like receptor  
 CC MOP2. MOP2 is a mouse receptor with pharmacological properties which  
 CC are dissimilar to the properties of classic opioid receptors such kappa,  
 CC delta, mu or sigma. It has been found that drugs of high abuse potential  
 CC or analgesic potency bind selectively to this receptor. This suggests  
 CC that this receptor could be important in the development of drugs to  
 CC treat addiction. Other opioid receptors isolated and produced such as the  
 CC novel mouse kappa and delta opioid receptors (Q75926-7) are useful for  
 CC the development of novel assays designed to select or improve substances,  
 CC capable of interacting with the opioid receptor proteins, for use in  
 CC diagnosis, drug design and therapeutic applications.  
 SQ Sequence 367 AA;

Query Match	53.28;	Score 1460;	DB 13;	Length 367;
Best Local Similarity	56.38;	Pred. No. 3.07e-124;		
Matches 180;	Conservative	67;	Mismatches 71;	Indels 2;
				Gaps 2;

Db	44	pjlkvrtivgilylavcigllgnclmvyvllrhtkmtkatniyifnlaladtllvlltlpf	103
QY	45	stalaiaitalysavcavglgnvlpwefgivrtytkltatnityifnlaladalattstlpe	104
Db	104	gtrdillgfwpfgnalcktviaidymftstftltamsvdryaachpiraldvrtssk	163
QY	105	qsakylmetwpefgellckavlsidyynmftsiftlltmmsvdrlylaavchpvakaldertpak	164
Db	164	agavnaivalasvvgvpvaimgsaqvedeeieclveipapqdywgpvfaiCIFlsfll	223
QY	165	aklNIClMwLASGVGPIMwMAVtQPRGAVwCMLQFPSPswyMDIvTKICVFLFAFVV	224
Db	224	pvlisvocyslmrlrlrgvrlsgrsrekdnrlrrlrlrlvllvvavfvgcwtbpvgvflvq	283
QY	225	pLlITVcYGlMLRLRsvRLLSGSkEKDRSLRITRMVllVVVGAFVwCwAPThIFVlW	284
Db	284	gl-gvqpgsetavailrfctalgyvnsclnpillyaflndenfkacfrkfccasalnremqv	342
QY	285	tlvDlNRDPLVVAALHLClALGYANSSlNPVlYAFldENfKRCfRQlCRlPCGRQEPGS	344
Db	343	sdrvr-siakdvglqcktse	361
QY	345	lRRPRQATTRERVTACTPSD	364

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Search completed: Tue Aug 26 14:44:55 1997
Job time : 22 secs.
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(TM)

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jul 18 08:10:10 1997; MasPar time 23.58 Seconds

Tabular output not generated. 291.549 Million cell updates/sec

Title: >US-08-700-356-1  
Description: (1-631) from US08700356.pep  
Perfect Score: 4516  
Sequence: 1 APLTAYSQQTRGLGCIITS.....THPTKYLACMSADLEVVT 631

Scoring table: PAM 150  
Gap 11

Searched: 92623 segs, 10896596 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq26  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19

Statistics: Mean 36.461; Variance 150.473; scale 0.242

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	4516	100.0	3010	4	R20111	Non-A, non-B viral ge	0.00e+00
2	4516	100.0	3010	4	R20091	Non-A, non-B viral ge	0.00e+00
3	4490	99.4	631	15	R82854	NS3 serine protease d	0.00e+00
4	4407	97.6	2354	8	R41435	PT-NANBH virus non-st	0.00e+00
5	4404	97.5	3014	10	R54099	NANBHV E1/E2 protein.	0.00e+00
6	4397	97.4	3014	7	R35207	Hepatitis C virus pro	0.00e+00
7	4389	97.2	916	18	R82693	Partial HCV non-struc	0.00e+00
8	4389	97.2	3010	18	R82694	Hepatitis C virus RNA	0.00e+00
9	4383	97.1	3010	14	R68864	Hepatitis C virus RNA	0.00e+00
10	4377	96.9	3010	13	R68622	HCV protein cleavable	0.00e+00
11	4360	96.5	923	18	R82696	HCV protein cleavable	0.00e+00
12	4359	96.5	3010	10	R53417	Blood transmissible N	0.00e+00
13	4337	96.0	3010	7	R34580	Human hepatitis C vir	0.00e+00
14	4327	95.8	2510	6	R29527	HCV antigen T7N1-30.	0.00e+00
15	4328	95.8	3011	8	R40120	HCV genomic amino aci	0.00e+00
16	4325	95.8	3011	12	R66995	Hepatitis C virus gen	0.00e+00
17	4322	95.7	2261	1	P90164	Peptide encoded by co	0.00e+00
18	4321	95.7	2301	1	P92047	Sequence encoded in t	0.00e+00
19	4322	95.7	2436	1	P92050	Sequence encoded in t	0.00e+00
20	4322	95.7	2462	1	P90288	Peptide encoded by co	0.00e+00

21	4324	95.7	3011	7	R34468	Encoded by full-lengt	0.00e+00
22	4322	95.7	3011	16	R90931	Hepatitis C virus pol	0.00e+00
23	4316	95.6	1188	6	R29870	HCV NS2-NS4 peptide M	0.00e+00
24	4319	95.6	2772	2	R08123	Hepatitis C virus pol	0.00e+00
25	4315	95.5	1786	1	P90158	Protein sequence of h	0.00e+00
26	4307	95.4	2435	5	R25135	HCV polypeptide 1.	0.00e+00
27	4309	95.4	3011	6	R31621	Hepatitis C virus (HC	0.00e+00
28	4308	95.4	3011	4	R21519	Compiled HCV sequence	0.00e+00
29	4306	95.3	3010	6	R30616	Polypeptide coded by	0.00e+00
30	4300	95.2	2436	5	R28582	HCV amino acid sequen	0.00e+00
31	4301	95.2	3011	8	R40119	HCV genomic amino aci	0.00e+00
32	4301	95.2	3011	14	R79232	HCV sequence.	0.00e+00
33	4296	95.1	2894	13	R70230	Composite hepatitis C	0.00e+00
34	4289	95.0	1766	1	P92041	Sequence encoded in t	0.00e+00
35	4292	95.0	2816	7	R34009	HCV-1 polypeptid.	0.00e+00
36	4289	95.0	2894	5	R24440	Composite HCV HC-J1/C	0.00e+00
37	4283	94.8	2955	2	R08124	Hepatitis C virus put	0.00e+00
38	4262	94.4	3011	4	R22154	NANBV Hutch c59 isola	0.00e+00
39	4258	94.3	687	14	R79223	PHCV150-encoded seque	0.00e+00
40	4258	94.3	1648	14	R79221	PHCV176-encoded seque	0.00e+00
41	4251	94.1	1188	6	R29660	HCV NS2-NS4 peptide M	0.00e+00
42	4251	94.1	3011	13	R67588	Hepatitis C virus gen	0.00e+00
43	4116	91.1	686	13	R66267	Hepatitis C virus (HC	0.00e+00
44	4116	91.1	840	3	R14349	HCV protease::hSOD le	0.00e+00
45	4116	91.1	841	13	R68547	HCV protease/hSOD fus	0.00e+00

ALIGNMENTS

RESULT	1	standard; Protein; 3010 AA.
ID	R20111	
AC	R20111;	
DT	01-MAY-1992	(first entry)
DE	Non-A, non-B viral genome product.	
KW	NANBV; vaccine; immunodiagnosis; antigen; antibody.	
OS	Non-A, non-B hepatitis virus.	
FH	key	Location/Qualifiers
FT	Protein	1..115
FT	/label= C	
FT	/note= "core protein"	116..191
FT	/label= M	
FT	/note= "matrix protein"	192..389
FT	/label= E	
FT	/note= "envelope protein"	390..729
FT	Protein	
FT	/label= NS1	730..1006
FT	Protein	
FT	/label= NS2	1007..1614
FT	Protein	
FT	/label= NS3	1615..1862
FT	Protein	
FT	/label= NS4a	1863..2012
FT	Protein	
FT	/label= NS4b	2013..3010
FT	Protein	
FT	/label= NS5	
FT	EP-463848-A.	
PN	02-JAN-1991.	305717.
PD	25-JUN-1991;	JP-167466.
PF	25-JUN-1991;	JP-230921.
PR	31-AUG-1990;	JP-305605.
PR	09-NOV-1990;	US-635451.
PR	28-DEC-1990;	JP-132090.
PR	08-MAY-1991;	JP-138493.
PR	14-MAY-1991;	JP-138493.
PA	(OSAV ) Osaka University.	
PI	Okayama H, Fuke I, Mori C, Takamizawa A, Yoshida I.	
DR	WPI; 92-009412/02.	
DR	N-PSDB; Q20268.	
PT	Non-A, non-B hepatitis virus (NANBV) particles - as vaccine, immuno-	
PT	diagnostics and screening agents for NANBV, and to remove NANBV from	

PT blood.  
PS Disclosure; Fig 2; 89pp; English.  
CC The sequence (SEQ ID NO 1) was deduced from several overlapping  
CC "BK" cDNA clones obtd. by "gene walking" using a cDNA clone isolated  
CC from a library prepd. from NANBV RNA. Antigenic polypeptides from  
CC the sequence can be used as immunoassay reagents, for screening  
CC donated blood, and as immunogens for vaccine prodn. Antibodies  
CC raised to the peptides can be used in immunoassays to detect or  
CC quantify NANBV antigens in liver tissue and blood. Preferred poly-  
CC peptides include residues 1-30, -115, or 2012; 47-77; 116-191;  
CC 192-207 or -298; 230-238 or -263; 287-300; 293-330; 390-729; 730-  
CC 1005; 1006-1614; 1384-1414; 1615-1862; 1737-1767; 1863-2012; and  
CC 2013-3010.  
CC The sequence is also disclosed in EP-464287 (SEQ ID NO 1).  
CC See R20091 for details of this specification.  
SQ Sequence 3010 AA;

Query Match 100.0%; Score 4516; DB 4; Length 3010;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1027 epltaysqgtrgllgcititsltgrdknqvegevqvstataqsfllatcvngvcwtvyhgag 1086  
QY 1 APITAYSQOTRGLLGCIITSLTRDKNOVEGEVQVSTATQSFLLATCVNGVCWTVYHGAG 60  
Db 1087 sktlaapkgpiltgmytnvdqdlvgwppkpgarsltptctcgssdlylvtrhadvipvrrrg 1146  
QY 61 SKTLAAPKGPITQMTYNVDQLVGWPKPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG 120  
Db 1147 dsrgslsprvsvylkssggpdlcpfghavgifraavctrgvakavdfrvvesmettmr 1206  
QY 121 DSRGSLSPRPVSVYKSSGGPDLCPFGHAVGIFRAAVCTRGVAKAVDFVVESMETTMR 180  
Db 1207 spvftdnssppavpqsfgvahlhaptgsgktkvpaaayaaggykxvlvlnpsvaatlfgga 1266  
QY 181 SPVFTDNSSPPAVPOSFQVAHLHAPTSGSKSTKVPAAAYAAGYKVLVLPNSVAATLGFGA 240  
Db 1267 ymskagidpnirtgvtitttgapvtystygfkladggcsggaydliidechstdstti 1326  
QY 241 YMSKAHGIDPNIRTGVRTITTGAPVTYSTYGFKLADGGCSGGAYDIIIDECHSTDSTTI 300  
Db 1327 lgiqtlvdgaetagarlvlatatppgsvtvphnieevalnsntgeipfykaiplaeair 1386  
QY 301 LGIGTVLDQAETAGARLVLATATPPGSVTVPHNIEEVALNSNTGEIPFYKAIPIEAIR 360  
Db 1387 ygrhlifchskkkcdelaaklsglginavayyrgldvsviptlgdvvvvatdaalmtygtg 1446  
QY 361 GGRHLIFCHSKKKCDELAAKLSGLGINAVAYYRGLDVSVIPTIGDVVVVATDALMTGYTG 420  
Db 1447 dfdsvidcntcvtqtvdfisldptftietttvpgdavsrsgrgrtgrgrylrvftpg 1506  
QY 421 DFDSVIDCNTCVTQTVDFISLDPTFTIETTTVPQDAVSRSQRGRGTGRGRGIRFVTPGE 480  
Db 1507 rpsgmfdssvlycecydagcawelytpaetsvrlraylntpglrvpcqdhlefweyftglt 1566  
QY 481 RPSGMFDSSVLYCECYDAGAWELYTPAETSVRLRAYLNTPGLPVCQDHLFEWESVFTGLT 540  
Db 1567 hidahflsqtkqagdnfpylvaygatvcaraqapppswdgmwkcilirlkptlhgptply 1626  
QY 541 HIDAHFLSQTKQAGDNFPYLVAYGATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLY 600  
Db 1627 rlgavqnevtlthpiktyinacmsadlevt 1657  
QY 601 RLGA VQNEVTLTHPIKTYINACMSADLEVT 631

RESULT 2  
ID R20091 standard; Protein; 3010 AA.  
AC R20091;  
DT 01-MAY-1992 (first entry)  
DE Non-A, non-B viral genome product.  
KW NANBV; vaccine; immunodiagnosis; antigen; antibody.  
OS Non-A, non-B hepatitis virus.

FH Key Location/Qualifiers  
FT Protein 1..115  
FT /label= C  
FT /note= "core protein"  
FT Protein 116..191  
FT /label= M  
FT /note= "matrix protein"  
FT Protein 192..389  
FT /label= E  
FT /note= "envelope protein"  
FT Protein 390..729  
FT /label= NS1  
FT Protein 730..1006  
FT /label= NS2  
FT Protein 1007..1614  
FT /label= NS3  
FT Protein 1615..1862  
FT /label= NS4a  
FT Protein 1863..2012  
FT /label= NS4b  
FT Protein 2013..3010  
FT /label= NS5  
FT EP-464287-A.  
PD 08-JAN-1992.  
PF 28-DEC-1990; 314371.  
PR 25-JUN-1990; JP-167466.  
PR 31-AUG-1990; JP-230921.  
PR 09-NOV-1990; JP-305605.  
PA (OSAU ) Osaka University.  
PI Okayama H, Fuke I, Mori C, Takamizawa A, Yoshida I.  
DR WPI; 92-009617/02.  
DR N-PSDB; Q21829.  
PT Non-A, non-B hepatitis virus (NANBV) particles - as vaccine, immuno-  
PT diagnostics and screening agents for NANBV, and to remove NANBV from  
PT blood.  
PS Claim 3; Fig 2; 89pp; English.  
CC The sequence was deduced from several overlapping "BK" cDNA clones  
CC obtd. by "gene walking" using a cDNA clone isolated from a library  
CC prepd. from NANBV RNA. Antigenic polypeptides from the sequence  
CC can be used as immunoassay reagents, for screening donated blood,  
CC and as immunogens for vaccine prodn. Antibodies raised to the  
CC peptides can be used in immunoassays to detect or quantify NANBV  
CC antigens in liver tissue and blood. Preferred polypeptides are  
CC include residues 1-30, -115, or 2012; 47-77; 116-191; 192-207 or  
CC -298; 230-238 or -263; 287-300; 293-330; 390-729; 730-1005; 1006-  
CC 1614; 1384-1414; 1615-1862; 1737-1767; 1863-2012; and 2013-3010.  
CC The sequence is also disclosed in EP-463848 (SEQ ID NO 1) in  
CC which a virus particle contg. antigens encoded by the sequence is  
CC claimed. See R20111 for details of this specification.  
SQ Sequence 3010 AA;

Query Match 100.0%; Score 4516; DB 4; Length 3010;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1027 epltaysqgtrgllgcititsltgrdknqvegevqvstataqsfllatcvngvcwtvyhgag 1086  
QY 1 APITAYSQOTRGLLGCIITSLTRDKNOVEGEVQVSTATQSFLLATCVNGVCWTVYHGAG 60  
Db 1087 sktlaapkgpiltgmytnvdqdlvgwppkpgarsltptctcgssdlylvtrhadvipvrrrg 1146  
QY 61 SKTLAAPKGPITQMTYNVDQLVGWPKPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG 120  
Db 1147 dsrgslsprvsvylkssggpdlcpfghavgifraavctrgvakavdfrvvesmettmr 1206  
QY 121 DSRGSLSPRPVSVYKSSGGPDLCPFGHAVGIFRAAVCTRGVAKAVDFVVESMETTMR 180  
Db 1207 spvftdnssppavpqsfgvahlhaptgsgktkvpaaayaaggykxvlvlnpsvaatlfgga 1266  
QY 181 SPVFTDNSSPPAVPOSFQVAHLHAPTSGSKSTKVPAAAYAAGYKVLVLPNSVAATLGFGA 240  
Db 1267 ymskagidpnirtgvtitttgapvtystygfkladggcsggaydliidechstdstti 1326



QY	241	YMSKAHGIDPNIRITGVRTITTTGAPVTVSTYGGKFLADGGCGGAYDIIICDECHSTDSTI	300
Db	1327	lgigtvlddaetagarlvvlatatppgsvtvphnueealvsnlntgeipfygkaipiealr	1386
QY	301	LGIGTVLDAQETAGARLVVATATPPGSVTVPHNIEEVALSNTGEIPFYGKAIPLEAIR	360
Db	1387	ggrhlifchskkkkcdelaaklsglginavayyrgldvsviptigdvvvvatdalmtytg	1446
QY	361	GGRHlIFCHSKKKKCDELAakLSGLGINAVAYYRGldVSVIPTIGDVVVVATdAlmTYTG	420
Db	1447	dfdsvidcntcvtqtvtvdfslcptfttiettpqdavsrsqrrgrtgrrgryrfvtpge	1506
QY	421	DFDSVIDCNTCVtQTlVDFSLDPTFTIETTVPQDAVSRSQRGRGTGRGRGIYRFVTPGE	480
Db	1507	rpsgmfdssvvlcecydagcawyeltpaetsvrlraylntpglpyvcqdhlefwestftgl	1566
QY	481	RPSGMFDSSVVLCECYDAGCawYELTPAETSVRLRAYlNTPGLPYVCQDHLefWESTFTGLT	540
Db	1567	hidahflisqtkaqadnfpylvayqatvcaraqapppswdgmwkelirlkptlthgptply	1626
QY	541	HIDAHflSQTkaQADNFPYlVAYQATVCARaQAPPPSWDGMWkELIRlkPTlHGPtPLY	600
Db	1627	rlgavgnevrlthpityimacmsadlevt	1657
QY	601	RLGAVQNEVRLTHPTIKYIMACMSADLEVT	631

ID	RESULT	3
AC	R82854; standard; protein; 631 AA.	
DT	04-APR-1996 (first entry)	
DE	NS3 serine protease domain.	
KW	NS3; serine protease; hepatitis C virus; HCV; NS4A; therapy.	
OS	Hepatitis C virus.	
FT	Key	
FT	Misc_difference 78	
FT	/note= "represented by Cal in the specification"	
FT	Misc_difference 132	
FT	/note= "represented by Cal in the specification"	
FT	Misc_difference 338	
FT	/note= "represented in the specification by Igu"	
FT	Misc_difference 454	
FT	/note= "represented in the specification by Aps"	
PN	W09522985-A1.	
PD	31-AUG-1995.	
PF	14-FEB-1995; IT0018.	
PR	23-FEB-1994; IT-RM0092.	
PA	(RICE-) 1ST RICEACHE BIOL MOLECOLARE ANGELETTI.	
PI	De Francesco R, Falla C, Tomei L;	
DR	WPI; 95-311381/40.	
PT	In vitro reproduction of hepatitis C virus NS3 protease activity -	
PT	by including the NS4A cofactor in the mixt., useful for screening	
PT	cpds. that inhibit NS3	
PS	Claim 6; Page 16-18; 26pp; English.	
CCC	This sequence represents the Hepatitis C virus (HCV) NS3 serine protease	
CC	domain. The NS3 serine protease domain requires NS4A (see R82855) as a	
CC	cofactor. Optimal serine protease activity is obtained when NS4A and NS3	
CC	are present in a 1:1 ratio. The cleavage site between these two proteins	
CC	on the HCV genome can be mutated so that the components remain covalently	
CC	bonded. These sequences are included in a composition that can be used	
CC	in an assay system. This assay system can be used to select compounds	
CC	that inhibit NS3 activity, e.g. potential therapeutic agents. NS4A can	
CC	be used for screening enzyme inhibitors.	
CC	Sequence 631 AA;	
CC	Sequence 631 AA;	

Query Match	99.48;	Score 4490;	DB 15;	length 631;
Best Local Similarity	99.48;	Pred. No. 0.00e+00;		
Matches 627;	Conservative	0;	Mismatches 4;	Indels 0;
				Gaps 0;

Dd 1 apitaysgqrlgllciltstlgrdknqvgegyvstatqsfllatcvngycwtyrhgag 60  
|||  
QY 1 apitaysqqlrgllgcilittslgrdknqvgegyvstatqsfllatcvngycwtyrhgag 60  
|||

D	b	61	sktlaapkgpbitgmvtuxdqdlvgwbpkppgarsltptctcgssdlylvtrhadviprrrg	120
Q	Y	61	SKTLAAPKGPITOMXTINVDQDLVGWPKPPGARS�TPCTCGSSDLYLVTRHADVIPRRRG	120
D	b	121	dsrgslsprpxsykkgssggpllpfghavgifraavctrivakavdvfpvesmetmr	180
Q	Y	121	DSRGSLSPRPVSYLKSGSGPLLPFGHAVGIFRAAVCTIRGVAKAVDEVFPVESMETMR	180
D	b	181	spvftdnssppavpgsfgyahlhaprtsgskstkvpaaayaagykvlvlnpsvaatlfgga	240
Q	Y	181	SPVFTDNSSPPAVPGSFQYAHLHAPRTSGSKSTKVPAAAYAAGYKVLVLPNSVAATLFGGA	240
D	b	241	ymskahgidpnirtgvrtilttgapvtystygkflladggsggagaydliidechstdstli	300
Q	Y	241	YMSKAHGIDPNIRTGVRTITTGAPVTYSTYGKFLADGGSGGAYDIIIDECHSTDSTLI	300
D	b	301	lgigtvldqaetagarilvlatatppgsvtyphnlexvalstgeipfygkaipieair	360
Q	Y	301	LGIGTVLDQAETAGARLVLATATPPGSVTYPHNIEVALSNTGEIPFYGKAIPIEAIR	360
D	b	361	ggrhlifchskkkodelaaklsglginaavayrrglvsviptligdvvvvatdalmtytg	420
Q	Y	361	GGRHLIFCHSKKKODELAKLSGLGINAAVAYRRGLVSVIPTIGDVVVVATDALMTYTG	420
D	b	421	dfdsvidcntcvttqtdvdfslldptftietttvpqxavsrsgrrgtgrgrgryrrftpg	480
Q	Y	421	DFDSVIDCNTCVTTQTDVDFSLDPTFTIETTVPQDAVSRSGRRGTGRGRGIRRYFTPG	480
D	b	481	rpsgmfdssvlceocydagcaweltpaetsvrlraylntpglpvcqdhlefvesvftgt	540
Q	Y	481	RPSGMFDSVYLCECYDAGCAMELTPAETSVRLRAYLNTPLPVCQDHLFVESVFTGT	540
D	b	541	hidahfistqtkgagdnfpylvayqatvcaraqapppswdqmwkclirklrptlhngptply	600
Q	Y	541	HIDAHFISQTKQAGDNFPYLVAYQATVCARAAQPPPSWDQMWKCLIRKLPTLHGPTPLY	600
D	b	601	rlgavqnevtlthpittkyimacmsadlevvt	631
Q	Y	601	RLGAVQNEVTLTHPITTKYIMACMSADLEVT	631

RESULT 4  
 ID R41435 standard; Protein; 2354 AA.  
 AC R41435;  
 DT 24-FEB-1994 (first entry)  
 DE PT-NANBH virus non-structural proteins.  
 KW Parenterally transmitted non A non B hepatitis; PT-NANBH; NS4;  
 KW hepatitis C virus; HCV; detection; diagnosis; antigen; vaccine;  
 OS amplification; primer; polymerase chain reaction; PCR.  
 OS Parenterally transmitted non A non B hepatitis virus.  
 PN W09317110-A.  
 PD 02-SEP-1993.  
 PF 19-FEB-1993; G00345.  
 PR 21-FEB-1992; GB-003803.  
 PA (WELL ) WELLCOME FOUND LTD.  
 PI Parker D, Rodgers BC;  
 DR WPI: 93-288415/36.  
 DR N-PSDB; Q46195.  
 PT New recombinant polypeptide for diagnosing hepatitis C - contains  
 PT three distinct antigens from different viral regions, also useful  
 PT in protective vaccines  
 PT Example 1; Page 43-53; 99pp; English.  
 PS The NS4 region from the 3' region of the PT-NANBH genome (Q46195)  
 CC is amplified by PCR using primers D224 and D226 (Q46196-97) and  
 CC the fragment (Q46198) is cloned into a vector and expressed in  
 CC infected insect cells. The recombinant virus (BHC-19) was able  
 CC to express the NS4 specific recombinant protein at low levels in  
 CC the infected insect cells.  
 CC If at least three different PT-NANBH antigens are used to screen  
 CC for PT-NANBH, the screening is much more sensitive as compared to  
 CC the use of only two PT-NANBH antigens. Pref. antigens are  
 CC described in Q46192-94. Two new antigenic regions of the  
 CC PT-NANBH genome are given in Q46198-99. Q46202 describes

CC an improved PT-NANBH recombinant polypeptide.  
SQ Sequence 2354 AA;

Query Match 97.6%; Score 4407; DB 8; Length 2354;  
Best Local Similarity 96.4%; Pred. No. 0.00e+00;  
Matches 608; Conservative 18; Mismatches 5; Indels 0; Gaps 0;

Db 211 apitaysqtrgllgciltsltgrdkngvegevgvstataqsfllatcvngvcwtvyhgag 270  
QY 1 APITAYSQQTREGLLGCIIITSLTGRDKNGVEGEVQVSTATQSFLLATCVNGVCWTVYHGAG 60  
Db 271 sktlaqpkgyvqmytnvdqdlvgwppaparsltptcgsdlylvtrhadviprrrg 330  
QY 61 SKTLAAPKGPITQMTNVDQDLVGWPKPGARSILTPCTCGSSDLYLVTRHADVIPVRRRG 120  
Db 331 dsrgslsprprvlylkgssggpllcpsghavgfiraavctrqvakavdifpvesmettvr 390  
QY 121 DSRGSLSPRPVSYLKGSSGGPILCPFGHAVGIFRAAVCTRGVAKAVDEVFVESMETTMR 180  
Db 391 spvftdnssppavpqsfgvahlhaptgsgkstrrvpaayaaggykvlvlnpsvaatlfgga 450  
QY 181 SPVFTDNSSPPAVPQSFQVAHLHAPTGSGKSTRVPAAYAAQGYKVLVLPNSVAATLGFGA 240  
Db 451 ymskahgvdnpnirsqvrllttgarpitystygrkfiadggcsggaydiilcdechstdsti 510  
QY 241 YMSKAHGIDPNIRIGVRITTTGAPVITYSTYGKFLADGGCSCSGAYDIILICDECHSTDSTTI 300  
Db 511 lgigtvlldaetagarlvlatatppgsvtvpbnpnievalsnatgeipfygkaipietik 570  
QY 301 LGIGTVLDQAETAGARLVLATATPPGSVTVPHNPNIEVALSNTGEIPFYGKAIPIEAIR 360  
Db 571 ggrhlifchskkkcdelaaklvglglnavayyrgldvsvipasgdvvnvatdalmtygtg 630  
QY 361 GGRHLIFCHSKKKCDELAAKLSGLGINAVAYYRGLDVSVIPTIGDVVNVAATDALMTGYTG 420  
Db 631 dfdsvidcntcvtqtvdffsldpfttielttvpqdvavsrqrrgrtgrgrgiyrfvapg 690  
QY 421 DFDSVIDCNTCVTQTVDFSLDPTFTIETTTPQDAVSRSQRRGTGRGRGIYRFVTPGE 480  
Db 691 rpsgmfdssvlylcecydagcaweyeltpaetsvrlraylnptgllpvcqdhlefweesvftgt 750  
QY 481 RPSGMFDSSVLYLCECYDAGCAWEELTPAETSVRLRAYLNPGLPVCQDHLEFWESVFTGLT 540  
Db 751 hvdaflisqtkqagdnfpylvayqatvcaraqapppswdqmwkcllrkptlrgptply 810  
QY 541 HIDAFLISQTKQAGDNFPYLVAYQATVCARAQAPPSPWDMWKCLIRLKP TLHGPTPLLY 600  
Db 811 rlgavgnevltlthpikfmacmsadlevt 841  
QY 601 RLGAVQNEVTLTHPITKYIMACMSADLEVT 631

RESULT 5  
ID R54099 standard; Protein; 3014 AA.  
AC R54099;  
DT 09-FEB-1995 (first entry)  
DE NANBHV E1/E2 protein.  
KW E1/E2 protein; non-A, non-B hepatitis virus; NANBHV; signal peptide;  
KW heterogenic; virus; transformation; insect cell; antigen; anti-NANBHV;  
KW antiboddy; hepatitis C virus; HCV; vaccine.  
OS Non-A, non-B hepatitis virus.  
FH Key Location/Qualifiers  
FT Peptide 832..847  
FT /note= "Peptide fragment not given in the specification,  
FT but encoded by the given cDNA sequence"  
FT Peptide 1296..1311  
FT /note= "Peptide fragment not given in the specification,  
FT but encoded by the given cDNA sequence"  
FT Peptide 1760..1775  
FT /note= "Peptide fragment not given in the specification,  
FT but encoded by the given cDNA sequence"  
FT Peptide 2688..2703  
FT /note= "Peptide fragment not given in the specification,

FT but encoded by the given cDNA sequence"  
PN J06141873-A.  
PD 24-MAY-1994.  
PF 13-MAR-1992; 089371.  
PR 13-MAR-1992; JP-089371.  
PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.  
DR WPI; 94-205030/25.  
DR N-PSDB; Q64175.  
PT Virus vector contg hepatitis C virus and signal sequence - useful  
PT in vaccines and in immunological detection  
PS Disclosure; page 7-19; 23pp; Japanese.  
CC This sequence represents the E1/E2 protein from non-A, non-B hepatitis  
CC virus (NANBHV). The cDNA encoding this sequence may be linked to a  
CC signal peptide (r54100) from a heterogenic virus so the the NANBH  
CC protein may be expressed by a transformed insect cell. This protein  
CC may be used as an antigen in the generation of anti-NANBHV antibodies.  
CC These antibodies may be used in a hepatitis C vaccine.  
SQ Sequence 3014 AA;

Query Match 97.5%; Score 4404; DB 10; Length 3014;  
Best Local Similarity 97.0%; Pred. No. 0.00e+00;  
Matches 612; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Db 1027 apitaysrtrgllgciltsltgrdkngvegevgvstataqsfllatcvngvcwtvyhgag 1086  
QY 1 APITAYSQQTREGLLGCIIITSLTGRDKNGVEGEVQVSTATQSFLLATCVNGVCWTVYHGAG 60  
Db 1087 sktlaqpkgyvqmytnvdqdlvgwppaparsltptcgsdlylvtrhadviprrrg 1146  
QY 61 SKTLAAPKGPITQMTNVDQDLVGWPKPGARSILTPCTCGSSDLYLVTRHADVIPVRRRG 120  
Db 1147 dnrgslsprprvlylkgssggpllcpsghavgfiraavctrqvakavdifpvesmettvr 1206  
QY 121 DSRGSLSPRPVSYLKGSSGGPILCPFGHAVGIFRAAVCTRGVAKAVDEVFVESMETTMR 180  
Db 1207 spvftdnssppavpqtfgvahlhaptgsgkstrvpaayatgykvlvlnpsvaatlfgga 1266  
QY 181 SPVFTDNSSPPAVPQSFQVAHLHAPTGSGKSTRVPAAYAAQGYKVLVLPNSVAATLGFGA 240  
Db 1267 ymskahgtdpnirtqvrllttgarpitystygrkfiadggcsggaydiilcdechstdsti 1326  
QY 241 YMSKAHGIDPNIRIGVRITTTGAPVITYSTYGKFLADGGCSCSGAYDIILICDECHSTDSTTI 300  
Db 1327 lgigtvlldaetagarlvlatatppgsvtvpbnpnievalsnatgeipfygkaipieaim 1386  
QY 301 LGIGTVLDQAETAGARLVLATATPPGSVTVPHNPNIEVALSNTGEIPFYGKAIPIEAIR 360  
Db 1387 ggrhlifchskkkcdelaaklsglglnavayyrgldvsviptsgdvvnvatdalmtygtg 1446  
QY 361 GGRHLIFCHSKKKCDELAAKLSGLGINAVAYYRGLDVSVIPTIGDVVNVAATDALMTGYTG 420  
Db 1447 dfdsvidcntcvtqtvdffsldpfttielttvpqdvavsrqrrgrtgrgrgiyrfvtpge 1506  
QY 421 DFDSVIDCNTCVTQTVDFSLDPTFTIETTTPQDAVSRSQRRGTGRGRGIYRFVTPGE 480  
Db 1507 rpsgmfdssvlylcecydagcaweyeltpaetsvrlraylnptgllpvcqdhlefweesvftgt 1566  
QY 481 RPSGMFDSSVLYLCECYDAGCAWEELTPAETSVRLRAYLNPGLPVCQDHLEFWESVFTGLT 540  
Db 1567 hvdaflisqtkqagdnfpylvayqatvcaraqapppswdqmwkcllrkptlrgptply 1626  
QY 541 HIDAFLISQTKQAGDNFPYLVAYQATVCARAQAPPSPWDMWKCLIRLKP TLHGPTPLLY 600  
Db 1627 rlgavgnevltlthpikymacmwadlevt 1657  
QY 601 RLGAVQNEVTLTHPITKYIMACMSADLEVT 631

RESULT 6  
ID R35207 standard; Protein; 3014 AA.  
AC R35207;  
DT 29-JUL-1993 (first entry)  
DE Hepatitis C virus protein.



RESULT 8  
ID R82694 standard; Protein; 3010 AA.  
AC R82694;  
DT 14-NOV-1996 (first entry)  
DE Partial HCV non-structural polypeptide.  
KW proteinase; hepatitis C virus; screening; inhibitor; proteolytic;  
KW identification; cleavage.  
OS Hepatitis C Virus.  
FH Key Location/Qualifiers  
FT Protein 898..1233  
FT /note= "partial proteinase; see R82692"  
FT Protein 992..1907  
FT /note= "partial proteinase; see R82693"  
PN J07184648-A.  
PD 25-JUL-1995.  
PE 05-FEB-1993; 018854.  
PR 07-FEB-1992; JP-022657.  
PR 18-SEP-1992; JP-249240.  
PR 04-DEC-1992; JP-325303.  
PA (KAEN/) KAENNO K.  
PA (SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.  
PA (SUMO) SUMITOMO METAL IND LTD.  
DR WPI; 95-287962/38.  
DR N-PSDB; T03960.  
PT An HCV proteinase active substance - which has activity as an  
PT anti-HCV agent and can be used to screen for proteinase inhibitors  
PS Disclosure; Page 39-48; 52pp; Japanese.  
CC The present sequence is a partial Hepatitis C Virus (HCV) polypeptide  
CC from the non-structural region. Partial proteinase sequences (R82692-  
CC 93) are contained within this sequence. The proteinases can be used as  
CC anti-HCV agents. They can also be used to screen cpds. for their ability  
CC to inhibit their proteolytic activity. In this way proteinase inhibitors  
CC can be identified.  
SQ Sequence 3010 AA;

Query Match 97.2%; Score 4389; DB 18; Length 3010;  
Best Local Similarity 96.0%; Pred. No. 0.00e+00;  
Matches 606; Conservative 19; Mismatches 6; Indels 0; Gaps 0;

Db 1027 apitaysgqtrgllgciltsltgrdknqvdgvyistatqsfllatcwnyrcwtvyhgag 1086  
|||  
QY 1 APITAYSQOTRGLGCGITTSITGRDKNQVEGEVQVSTATQSFLLATCVNGVCWTVYHGAG 60  
Db 1087 sktlagpkxpitgmylnvdqdlvgwpaprgarsmtptcggssdlylvtrnadvvpyrrrg 1146  
|||  
QY 61 SKTLAAPKGPITQMYTNVDQDLVGWPKPPGARSILTPCTCGSSDLYLVTRHADVIPVRRRG 120  
Db 1147 dsrgslsprpisylykssggpplcpsgnhvvgifraavctrvgakavdflpresmettmr 1206  
|||  
QY 121 DSRGSLSPRPVSYLKSSGGPFLCPFGHAGVIFRAAVCTRGVAKAVDEVPESMETTMR 180  
Db 1207 spvftdnssppavpqrftgvahlhaprgtsqgstkvpaayaagykvlvlnpsvaatlqfiga 1266  
|||  
QY 181 SPVFTDNSSPPAVPQSFQVAHLHAPTSGSKSTKVPAAAYAQQGYKVLVLPNSVAATLGFGA 240  
Db 1267 ymskahgiepnirtgyrtlttggpitystyckfladggcsggaydliidechstdstti 1326  
|||  
QY 241 YMSKAHGIDPNIRITGVRTTTGAPVITYSTYGFELADGGCSGAYDIIICDECHSTDSTTI 300  
Db 1327 lgigtvlldqaetagarlvlatatppgsitvphnleeralnsntgeipfygkaipleak 1386  
|||  
QY 301 LGIGTVLDQAETAGARLVVLAATPPGSVTPHPNIEVALSNTGEIPFYGKAIPLEAIR 360  
Db 1387 ggrhlifchskkkcdelaakltglgnavayrgldvsviptsgdvvvvatdalmntgftg 1446  
|||  
QY 361 GGRHLIFCHSKKKCDELAARLSGLGINAVAYRGLDVSVIPTIGDVVVVATDALMTGYTG 420  
Db 1447 dfdsvidentcvtqtvdfsldpftiettltpdavsraqrgtrgrgsiyrftypge 1506  
|||  
QY 421 DFDSVIDCNTCVTQTVDFSLDPFTTETTTVPQDAVSRSGRGRGTGRGRGIXRFVTPGE 480

Db 1507 rpsgmfdssvlcecydagcayeltptaetsvrlraylntpglpvcqdhlefesvftgtlt 1566  
|||  
QY 481 RPSGMFDDSSVLCCECYDAGCAWTELLTPAETSVRRLRAYLNTPGLPVCQDHLFEWESVFTGLT 540  
Db 1567 hidahflsgtkqagdnlpylrayqatvcaraqappswdgmwkcilirkpptlhgppilly 1626  
|||  
QY 541 HIDAHFLLSGTKQAGDNFPYLYAYQATVCARAQAPPSPWDQMKCLIRKPTLHGPPILLY 600  
Db 1627 rlgavqnevltlthpitykymacsadlevt 1657  
|||  
QY 601 RLGAVQNEVTLTHPITKYIMACMSADLEVT 631

RESULT 9  
ID R68864 standard; Protein; 3010 AA.  
AC R68864;  
DT 06-DEC-1995 (first entry)  
DE Hepatitis C virus RNA helicase.  
KW Hepatitis C virus; HCV; non-A non-B; helicase gene; RNA helicase;  
KW baculovirus; recombinant production.  
OS Hepatitis C virus.  
FH Key Location/Qualifiers  
FT Region 196..198  
FT /label= N-linked glycosylation site  
FT Region 209..211  
FT /label= N-linked glycosylation site  
FT Region 234..236  
FT /label= N-linked glycosylation site  
FT Region 250..252  
FT /label= N-linked glycosylation site  
FT Region 305..307  
FT /label= N-linked glycosylation site  
FT Region 325..327  
FT /label= N-linked glycosylation site  
FT Region 417..419  
FT /label= N-linked glycosylation site  
FT Region 423..425  
FT /label= N-linked glycosylation site  
FT Region 430..432  
FT /label= N-linked glycosylation site  
FT Region 448..450  
FT /label= N-linked glycosylation site  
FT Region 532..534  
FT /label= N-linked glycosylation site  
FT Region 556..558  
FT /label= N-linked glycosylation site  
FT Region 576..578  
FT /label= N-linked glycosylation site  
FT Region 623..625  
FT /label= N-linked glycosylation site  
FT Region 645..647  
FT /label= N-linked glycosylation site  
FT Region 1213..1215  
FT /label= N-linked glycosylation site  
FT Region 1255..1257  
FT /label= N-linked glycosylation site  
FT Region 2041..2043  
FT /label= N-linked glycosylation site  
FT Region 2077..2079  
FT /label= N-linked glycosylation site  
FT Region 2240..2242  
FT /label= N-linked glycosylation site  
FT Region 2788..2790  
FT /label= N-linked glycosylation site  
PN J06319583-A.  
PD 22-NOV-1994.  
PE 18-SEP-1992; 249241.  
PR 18-SEP-1992; JP-249241.  
PA (SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.  
DR WPI; 95-040330/06.  
DR N-PSDB; O81559.  
PT Expression of hepatitis C virus helicase gene in baculovirus -  
PT useful for large scale prodn. of RNA helicase.



PS Claim 1; Fig 1-4; 9pp; Japanese.  
CC 081559 encodes R68864 hepatitis C virus (HCV) RNA helicase. The  
CC DNA was used in the construction of an expression vector, which  
CC was used to transform a baculovirus host. The transformed  
CC baculovirus could then be used for the recombinant prodn. of  
CC HCV RNA helicase.  
SQ Sequence 3010 AA;

Query Match 97 1%; Score 4383; DB 14; Length 3010;  
Best Local Similarity 95.9%; Pred. No. 0.00e+00;  
Matches 605; Conservative 20; Mismatches 6; Indels 0; Gaps 0;

Db 1027 apitaysqtrgllgcitstltgrdkngvqgvlstatqsfllatcvngvcwtvyhgag 1086  
QY 1 APITAYSQOTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTYHGAG 60  
Db 1087 sktlaagpkapitgmtylnvdqdlvgwpappgarmtpctcgssdlylvtrhadvpyrrrg 1146  
QY 61 SKTLAAPKGPITQMTYNVDQDLVGWPKPPGARSILTPCTCGSSDLVLTNRHADYIPVRRRG 120  
Db 1147 dsrgslsprpisyllkssggpplcpsghvvgifraavctrgrvakavdflpvesmettmr 1206  
QY 121 DSRGSLSPRPVSYLKSSGGPILCPFGHAGVIFRAAVCTRGVAKAVDFVYESMETIMR 180  
Db 1207 spvftdnssppavpqtffqvahlhaptsgskstkypaayaagkykvlvlnpsvaatlfgga 1266  
QY 181 SPVFTDNSSPPAVPQSFQVAHLHAPTSGSKSTKYPAAAYAOGYKVLVLPNSVAATLFGGA 240  
Db 1267 ymskahgiepnirtgvtlttggpitystyckfladggcgsgaydiilicdechststti 1326  
QY 241 YMSKAHGIDPNIRTKVRIITTGAPVTVSTYCKFLADGGCGSGAYDIILICDECHSTDSTTI 300  
Db 1327 lgigtvlqgaetagarlvlatatpssitvphnieevalsntgeipfygkaipieaik 1386  
QY 301 LGIGTVLDQAGTAGARLVLATATPPGSVTVPHNIEVALSNTGEIPFYGKAIPIEAIR 360  
Db 1387 ggrhlifchskkkcdelaakltgiglnavayyrgldvsviptsgdvvvvatdalmgtgtg 1446  
QY 361 GGRHLIFCHSKKKCDELAAKLSGLGNNAVAYYRGLDVSVIPTIGDVVVVATDALMTGTG 420  
Db 1447 dfdsvidcntcvtqtvdfsldpfttietttlpqdavsrarrrgrtgrgsiyrftpgae 1506  
QY 421 DFDSVIDCNTCVTQTVDFSLDPTFTTETTTVPQDAVSRSQRGRGRGRIYRFVTPGE 480  
Db 1507 rpsgmfdssvlcecydagcawyeltpaetsvrlraylntpglpvcqdhlefesvftgt 1566  
QY 481 RPSGMFDSSVLCCECYDAGCAMELTTPAETSVRLRAYLNTPGLPVCQDHLFEWESVFTGLT 540  
Db 1567 hidahflsqtkqagdnlpylvayqatvcaraqappswdgmwkcilrlkptlhgptpily 1626  
QY 541 HIDAHFLSQTKQAGDNFPYLVAYQATVCAARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600  
Db 1627 rlgavqnevtllhptikyimamsadlevt 1657  
QY 601 RLGAVQNEVTLTHPTIKYIMACMSADLEVVT 631

RESULT 10  
ID R68622 standard; Protein; 3010 AA.  
AC R68622;  
DT 16-OCT-1995 (first entry)  
DE HCV protein cleavable with new serine proteinase.  
KW proteinase; serine; cleavage; hepatitis C virus; HCV.  
OS Hepatitis C Virus.  
FH Key Location/Qualifiers  
FT Cleavage\_site 2419..2420  
FT /note= "Serine protease cleavage site"  
PN J06315377-A.  
PD 15-NOV-1994.  
PE 06-MAY-1993; 105666.  
PR 06-MAY-1993; JP-105666.  
PA (KAEN/) KAENNO K.  
PA (SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.

PA (SUMQ ) SUMITOMO METAL IND LTD.  
DR WPI; 95-032330/05.  
DR N-PSDB; Q80498.  
PT New HCV-originated proteinase active substance - used for  
PT site-specific cleavage by an intermolecular reaction and the  
PT purification thereof  
PS Disclosure; Page 10-19; 23pp; Japanese.  
CC This protein from HCV (hepatitis C virus) (encoded by Q80498) is  
CC cleaved between amino acids 2419 and 2420, by a new serine protease,  
CC contg. the sequence of R68621. The proteinase is purified as a fused  
CC product with the dihydrofolate reductase protein by using a methotrexate  
CC column. It can be used for the development of an inhibitor for HCV  
SQ Sequence 3010 AA;

Query Match 96.9%; Score 4377; DB 13; Length 3010;  
Best Local Similarity 95.9%; Pred. No. 0.00e+00;  
Matches 605; Conservative 19; Mismatches 7; Indels 0; Gaps 0;

Db 1027 apitaysqtrgllgcitstltgrdkngvqgvlstatqsfllatcvngvcwtvyhgag 1086  
QY 1 APITAYSQOTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTYHGAG 60  
Db 1087 sktlaagpkapitgmtylnvdqdlvgwpappgarmtpctcgssdlylvtrhadvpyrrrg 1146  
QY 61 SKTLAAPKGPITQMTYNVDQDLVGWPKPPGARSILTPCTCGSSDLVLTNRHADYIPVRRRG 120  
Db 1147 dsrgslsprpisyllkssggpplcpsghvvgifraavctrgrvakavdflpvesmettmr 1206  
QY 121 DSRGSLSPRPVSYLKSSGGPILCPFGHAGVIFRAAVCTRGVAKAVDFVYESMETIMR 180  
Db 1207 spvftdnssppavpqtffqvahlhaptsgskstkypaayaagkykvlvlnpsvaatlfgga 1266  
QY 181 SPVFTDNSSPPAVPQSFQVAHLHAPTSGSKSTKYPAAAYAOGYKVLVLPNSVAATLFGGA 240  
Db 1267 ymskahgiepnirtgvtlttggpitystyckfladggcgsgaydiilicdechststti 1326  
QY 241 YMSKAHGIDPNIRTKVRIITTGAPVTVSTYCKFLADGGCGSGAYDIILICDECHSTDSTTI 300  
Db 1327 lgigtvlqgaetagarlvlatatpssitvphnieevalsntgeipfygkaipieaik 1386  
QY 301 LGIGTVLDQAGTAGARLVLATATPPGSVTVPHNIEVALSNTGEIPFYGKAIPIEAIR 360  
Db 1387 ggrhlifchskkkcdelaakltgiglnavayyrgldvsviptsgdvvvvatdalmgtgtg 1446  
QY 361 GGRHLIFCHSKKKCDELAAKLSGLGNNAVAYYRGLDVSVIPTIGDVVVVATDALMTGTG 420  
Db 1447 dfdsvidcntcvtqtvdfsldpfttietttlpqdavsrarrrgrtgrgsiyrftpgae 1506  
QY 421 DFDSVIDCNTCVTQTVDFSLDPTFTTETTTVPQDAVSRSQRGRGRGRIYRFVTPGE 480  
Db 1507 rpsgmfdssvlcecydagcawyeltpaetsvrlraylntpglpvcqdhlefesvftgt 1566  
QY 481 RPSGMFDSSVLCCECYDAGCAMELTTPAETSVRLRAYLNTPGLPVCQDHLFEWESVFTGLT 540  
Db 1567 hidahflsqtkqagdnlpylvayqatvcaraqappswdgmwkcilrlkptlhgptpily 1626  
QY 541 HIDAHFLSQTKQAGDNFPYLVAYQATVCAARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600  
Db 1627 rlgavqnevtllhptikyimamsadlevt 1657  
QY 601 RLGAVQNEVTLTHPTIKYIMACMSADLEVVT 631

RESULT 11  
ID R82696 standard; Protein; 923 AA.  
AC R82696;  
DT 14-NOV-1996 (first entry)  
DE HCV partial proteinase.  
KW proteinase; hepatitis C virus; screening; inhibitor; proteolytic;  
KW identification; cleavage.  
OS Hepatitis C Virus.  
PN J07184648-A.

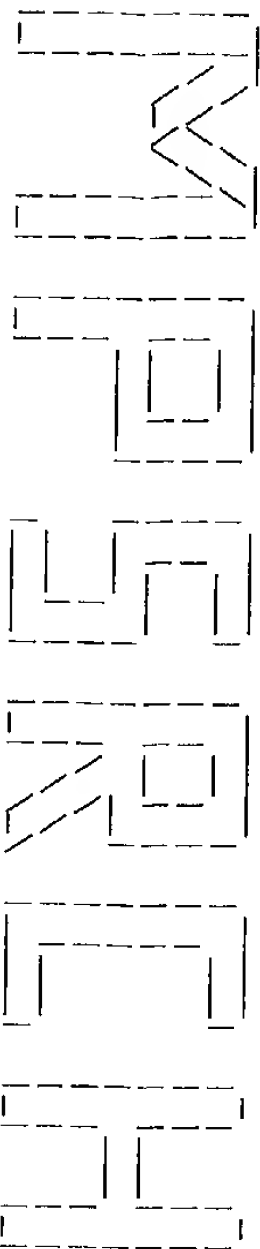
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PD 25-JUL-1995.  
PF 05-FEB-1993; 018854.  
PR 07-FEB-1992; JP-022657.  
PR 18-SEP-1992; JP-249240.  
PR 04-DEC-1992; JP-325303.  
PA (KAEN/) KAENNO K.  
PA (SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.  
PA (SUMO) SUMITOMO METAL IND LTD.  
DR WPI; 95-287962/38.  
DR N-PSDB; T03985.  
PT An HCV proteinase active substance - which has activity as an  
PT anti-HCV agent and can be used to screen for proteinase inhibitors  
PS Example 2; Page 33-39; 52pp; Japanese.  
CC The present sequence (contg. R82693) is that of a partial proteinase  
CC isolated from Hepatitis C virus (HCV). The proteinase can be used  
CC as an anti-HCV agent. It can also be used to screen cpds. for their  
CC ability to inhibit its proteolytic activity. In this way proteinase  
CC inhibitors can be identified.  
SQ Sequence 923 AA;

Query Match 96.5%; Score 4360; DB 18; Length 923;  
Best Local Similarity 95.2%; Pred. NO. 0.00e+00;  
Matches 601; Conservative 23; Mismatches 7; Indels 0; Gaps 0;

Db 38 apitaysqtrgllgcitsltgrdknqvdegyvlistatqsfllatcvmgvcwtvyhgag 97  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 1 APITAYSQOTRGLGCLITSLTRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG 60  
  
Db 98 sktlagpkpkitqmylnvdqdlvgwppaprgarsmtptcgsdlylvtrhadvipvrrrg 157  
||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 61 SKTLAPKGPITQMTNMDQLVGPMPKPGARSLTPTCTGSSDLVLTTRHADYLPVRRRG 120  
  
Db 158 dsrgslsprvpvpylkysggplvcpsghvvgifraavctrigvakavdfipvesmetmr 217  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 121 DSRGSLSPRPVSYLKSSGGPLLCFPGHAVGIFRAVCTRGVAKAVDFVPVESMETMR 180  
  
Db 218 spvltlnssppavpqtfgvahlnhaptsgskstkvpaaayaagrykvlvlnpsvaatlfgfga 277  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 181 SPVFTDNSSPPAVPQSFQVAHLHAPTSGSGSKSTKVPAAYAAQGYKVLVLPNSVAATLFGGA 240  
  
Db 278 ymskahgiepnirtgvrtiltggpitystyckfladggcsggagaydliidechnstdstli 337  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 241 YMSKAHGIDPNIRTGVRTTGTGAPVTYSTYCKFLADGGCSGGAYDIIICDECHSTDSTTI 300  
  
Db 338 lgitvldqaetagarlvlatatppgsityphnpnievalsntgeipfygkaipiealk 397  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 301 LGITVLDQAEETAGARLVVLAATPPGSVTVPHPNIEVALSNTGEIPFYGKAIPIEAIR 360  
  
Db 398 ggrhlffchskkkcdelaakltgllnavayyrgldvsvlptsgdvvvvatdalmgtfg 457  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 361 GGRHLFFCHSKKKCDELAALSGIGINAVAYYRGLDVSVLPTIGDVVVVATDALMGTGTG 420  
  
Db 458 dfdsvidentcvtqtvdflqptftietlllpqdavsrarrrtgrgrsilyrfvtpge 517  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 421 DFDSVIDCNTCVTQTVDLPTFTIETTTVPQDAVSRSGRRGRTGRRGRTYRFVTPGE 480  
  
Db 518 rpsgmfdssvlyceydagcawyeltpaettvrlraylnpqlpvcqdhlefesvftgl 577  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 481 RPSGMFDSSVLYCEYDAGCAMELTPAETSVRLRAYLNPGLPVCQDHLFEWESVFTGLT 540  
  
Db 578 hidahfistkqagdnfpylvaygatvcaraqapppswdgmwkcilrlkptlhgptply 637  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 541 HIDAHFISQTKQAGDNFPYLVAYQATVCARAQADPPSWDQMWKCLIRLKP TLHGPTPLY 600  
  
Db 638 rlgavqneitlthpikfvmacmsadlevvt 668  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 601 RLGA VQNEVTLTHPTIKYIMACMSADLEVV 631

RESULT 12  
ID R53417 standard; Protein; 3010 AA.  
AC R53417;  
DT 17-JAN-1995 (first entry)



(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPSrch\_n n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Tue Aug 26 09:12:13 1997; MasPar time 2128.91 Seconds  
Tabular output not generated. 1172.094 Million cell updates/sec

Title: >US-08-292-694A-3  
Description: (1-2272) from US08292694A.seq  
Perfect Score: 2272  
N.A. Sequence: 1 CACGCGCGCCCATGGAGCTG.....CTTCCACACACTGTGGCA 2272  
Comp: GTGCGCGCGGTACCTCGAC.....GAAAGTGTGTACACCCCGT

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 362067 seqs, 549138275 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database:

emb1-new3  
1:BC1 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV  
9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC  
17:VIR

Database:

genbank99  
18:BC11 19:BC12 20:BC13 21:BC14 22:BC15 23:BC16 24:BC17  
25:BC18 26:BC19 27:BC110 28:BC111 29:GEN1 30:GEN2  
31:GEN3 32:HTG1 33:HTG2 34:HTG3 35:INV1 36:INV2 37:INV3  
38:INV4 39:INV5 40:INV6 41:INV7 42:INV8 43:INV9 44:INV10  
45:INV11 46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3  
52:VRT4 53:PAT1 54:PAT2 55:PAT3 56:PAT4 57:PAT5 58:PHG  
59:PLN1 60:PLN2 61:PLN3 62:PLN4 63:PLN5 64:PLN6 65:PLN7  
66:PLN8 67:PLN9 68:PLN10 69:PLN11 70:PRI1 71:PRI2  
72:PRI3 73:PRI4 74:PRI5 75:PRI6 76:PRI7 77:PRI8 78:PRI9  
79:PRI10 80:PRI11 81:PRI12 82:PRI13 83:PRI14 84:PRI15  
85:ROD1 86:ROD2 87:ROD3 88:ROD4 89:ROD5 90:ROD6 91:ROD7  
92:ROD8 93:STR 94:SYN 95:UNA 96:VRL1 97:VRL2 98:VRL3  
99:VRL4 100:VRL5 101:VRL6 102:VRL7 103:VRL8 104:VRL9  
105:VRL10

Database:

genbank-new3  
106:BC1 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV  
112:MAM 113:VRT 114:PHG 115:PLN 116:PRI1 117:PRI2  
118:ROD 119:SYN 120:UNA 121:VRL  
u-emb150\_99  
122:part1

Database:

Statistics: Mean 12.005; Variance 5.716; scale 2.100

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2272	100.0	2272	88	MUSDELOPRE	Mouse delta opioid re	0.00e+00
2	2095	92.2	2203	92	S66181	delta opiate receptor	0.00e+00
3	2053	90.4	2219	88	MUSDELTO	Mus musculus delta-op	0.00e+00
4	1705	75.0	1834	92	S65335	delta opioid receptor	0.00e+00
5	1705	75.0	1835	88	MUSDOPRCP	Mouse delta-opioid re	0.00e+00
6	1124	49.5	1366	92	RNU00475	Rattus norvegicus Spr	0.00e+00
7	1119	49.3	1418	91	RATRORA	Rat mRNA for rat opio	0.00e+00
8	889	39.1	1773	77	HSU07882	Human delta opiate re	0.00e+00
9	878	38.6	1136	77	HSU10504	Human delta opiate re	0.00e+00
10	552	24.3	686	48	SSU71149	Sus scrofa delta opio	0.00e+00
11	365	16.1	1401	91	RATMOPID	Rat mu opioid recepto	5.32e-282
12	365	16.1	1448	92	RNU02083	Rattus norvegicus mu-	5.32e-282
13	365	16.1	1586	91	RATMORA	Rattus norvegicus mu	5.32e-282
14	363	16.0	2135	91	RATMUORA	Rattus norvegicus Mu	3.10e-280
15	361	15.9	2397	91	RATRORB	Rat mRNA for rat opio	1.81e-278
16	359	15.8	1367	92	RNU35424	Rattus norvegicus mu	1.06e-276
17	357	15.7	1610	87	MMU26915	Mus musculus mu opioi	6.16e-275
18	354	15.6	356	92	S81965	delta opioid receptor	2.73e-272
19	354	15.6	1415	112	BTU89677	Bos taurus mu opioi	2.73e-272
20	354	15.6	1415	10	BTU89677	Bos taurus mu opioi	2.73e-272
21	355	15.6	2229	87	MMU19380	Mus musculus mu opioi	3.58e-273
22	348	15.3	2302	48	PIGMOPR	Sus scrofa (clone id7	5.37e-267
23	338	14.9	1610	82	HUMOPIODA	Homo sapiens opioid r	3.50e-258
24	336	14.8	1473	77	HSU12569	Human mu opioid recep	2.02e-256
25	336	14.8	2162	82	HUMORLX	Human Mu opiate recep	2.02e-256
26	326	14.3	2205	48	SSU72758	Sus scrofa orphanin F	1.29e-247
27	321	14.1	1252	82	HUMOPRLP	Homo sapiens (clone A	3.22e-243
28	321	14.1	1973	75	HSORL1	H. sapiens mRNA for OR	3.22e-243
29	321	14.1	2534	77	HSU30185	Human orphan opioid r	3.22e-243
30	303	13.3	1154	77	HSU17298	Human kappa opioid re	2.08e-227
31	303	13.3	1604	82	HUMOPRK1B	Homo sapiens (clone d	2.08e-227
32	301	13.2	1182	77	HSU11053	Human kappa opioid re	1.18e-225
33	295	13.0	720	92	S77863	mu-opioid receptor MO	2.16e-220
34	291	12.8	1288	92	S81111	kappa-opioid receptor	6.90e-217
35	291	12.8	1410	89	MUSKAPOPRE	Mouse kappa opioid re	6.90e-217
36	286	12.6	1733	85	CPU04092	Cavia porcellus Hartl	1.65e-212
37	282	12.4	1253	91	RATOPRE	Rattus norvegicus opi	5.22e-209
38	282	12.4	1452	92	RNU01913	Rattus norvegicus Spr	5.22e-209
39	282	12.4	1567	91	RATOPRECEP	Rat opioid receptor f	5.22e-209
40	282	12.4	1817	91	RATRORC	Rat mRNA for opioid r	5.22e-209
41	282	12.4	2354	92	RNU07871	Rattus norvegicus Spr	5.22e-209
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43	279	12.3	1358	90	RATKORA	Rat kappa opioid rece	2.19e-206
44	279	12.3	2094	90	RATKOR1B	Rattus norvegicus kap	2.19e-206
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ALIGNMENTS

RESULT 1  
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DEFINITION Mouse delta opioid receptor mRNA, complete cds.  
ACCESSION L11064  
NID g348246  
KEYWORDS delta opioid receptor.  
SOURCE Mus musculus (library: Clontech #ML1036a) brain cDNA to mRNA.  
ORGANISM Mus musculus

REFERENCE  
1 (bases 1 to 2272)  
Yasuda,K., Raynor,K., Kong,H., Breder,C.D., Takeda,J., Reisine,T.  
and Bell,G.I.  
Cloning and functional comparison of kappa and delta opioid  
receptors from mouse brain  
Proc. Natl. Acad. Sci. U.S.A. 90, 6736-6740 (1993)

TITLE

JOURNAL  
MEDLINE  
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BASE COUNT	485 a	665 c	650 g 472 t
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KEYWORDS  
SOURCE mice NG108-15 cells.  
ORGANISM Mus sp.  
REFERENCE 1 (bases 1 to 1834)  
AUTHORS Keith,D.E., Jr., Anton,B. and Evans,C.J.  
TITLE Characterization and mapping of a delta opioid receptor clone from  
NG108-15 cells  
JOURNAL Proceedings of the Western Pharmacology Society 36, 299-306 (1993)  
MEDLINE 93391482  
REMARK GenBank staff at the National Library of Medicine created this  
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Query Match 75.0%; Score 1705; DB 92; Length 1834;  
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LOCUS MUSDOPRCP 1835 bp mRNA  
DEFINITION Mouse delta-opioid receptor (DOR-1) mRNA sequence.  
ACCESSION L07271  
NID g553906  
KEYWORDS delta-opioid receptor.  
SOURCE Mus musculus cdna to mRNA.  
ORGANISM Mus musculus



Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1835)  
AUTHORS Evans,C.J., Keith,D., Magendzo,K., Morrison,H. and Edwards,R.H.  
TITLE Cloning of a delta opioid receptor by functional expression  
JOURNAL Science 258, 1952-1955 (1992)  
MEDLINE 93110361

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source location/Qualifiers  
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DEFINITION	Rattus norvegicus Sprague-Dawley delta opioid receptor (dor1) mRNA, complete cds.				
ACCESSION	U00475				
NID	9403488				
KEYWORDS					
SOURCE	Norway rat.				
ORGANISM	Rattus norvegicus				
	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.				
REFERENCE	1 (bases 1 to 1366)				
AUTHORS	Abood, M.E.				
TITLE	Molecular cloning and expression of a rat delta opioid receptor from rat brain				
JOURNAL	J. Neurosci. Res. 27, 714-719 (1994)				
REFERENCE	2 (bases 1 to 1366)				
AUTHORS	Abood, M.E.				
TITLE	Direct Submission				
JOURNAL	Submitted (09-AUG-1993) Mary E. Abood, Pharmacology and Toxicology, Medical College of Virginia/Virginia Commonwealth University, 1112 E. Clay St., Richmond, VA 23298, USA				
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QY	126	ggagcccgtagtgctctgcctctgcctccctgcgtctctggccatcgccatcacgcgccttactcgct	185		
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QY	306	accagcgaactgcctctccagagcgcgcaagtacactgatggaacgctggcgttcgagag	365		
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QY	426	CTCACCATGATGAGCGTGTGACCGGCTACATTGCTGTGCCATCCTGTCAAAGCCCTGGAC				485
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QY	666	CTCTTTGCTTCGTGTGTGTCGGATCCTCATCATCAACGGGTGTGCTATGGCCTCATGTACTG				725
Db	763	cgcctgcgcagcgtgcgcctgtctgcgcgtcccaaggaagaaagcgcagccctgcgcgc				822
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Db	1003	gccttcctgacagaaactcaagcgcgtcttcgcgcagcctctgtcgcgcgcctgtgcgc				1062
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QY	1026	CGCCAAAGAACCCGCGCAGTCTCCGTCGTCCCGCCAGGCCAACACGCGGTGAGCGTCACT				1085
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QY	1146	CCTTAACGCCCTCCCAAGTGAAGTATCCAGAGGCCACACCGAGCTCCCTGGAGGGCT				1205
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KEYWORDS G-protein coupled receptor; rat opioid receptors; transmembrane protein.

SOURCE Rattus norvegicus (strain Wistar) adult brain cDNA to mRNA, clone pROR10.

ORGANISM Rattus rattus

REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.

1 (bases 1 to 1418)

REFERENCE Fukuda,K., Kato,S., Mori,K., Iwabe,N., Miyata,T., Nishi,M. and Takeshima,H.

TITLE Primary structures and expression from cDNAs of rat opioid receptor delta- and mu-subtypes

JOURNAL FEBS Lett. 327, 311-314 (1993)

MEDLINE 93351652

REFERENCE 2 (sites)

AUTHORS Wang,J.B., Johnson,P.S., Imai,Y., Persico,A.M., Ozenberger,B.A., Eppler,C.M. and Uhl,G.R.

TITLE CDNA cloning of an orphan opiate receptor gene family member and its splice variant

JOURNAL FEBS Lett. 348, 75-79 (1994)

MEDLINE 94298959

COMMENT Submitted (03-JUN-1993) to DDBJ by: Hiroshi Takeshima International Institute for Advanced Studies c/o Shimadzu Corporation N-80 1 Nishinokyo-Kuwarehara-cho Kyoto 604 Japan

Phone: 075-823-1208

Fax: 075-811-8186.

FEATURES

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QY |||||||

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Db 700 acgctccagttccccagccccagctgtagctggagacactgtgaccaagatctgcgtttc 759

QY |||||||

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Db 760 ctcttcgcttcgtgtgtgccattctcatcatcacaccgtgtgtatgtgcctcatgtcgtg 819

QY |||||||

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QY |||||||

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QY |||||||

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QY |||||||

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Db 1000 ggcgtgcacttgtgtcattgtgcgtctgggtctacgccaacagcagccctcaaccggttctctac 1059

QY |||||||

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RESULT 8



[illegible]

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REFERENCE AUTHORS TITLE JOURNAL MOL. Pharmacol. 46 (6), 1015-1021 (1994)			
MEDLINE	95107267		



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REFERENCE 2 (bases 1 to 1136)
AUTHORS Kieffer,B.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1994) Brigitte Kieffer, Ecole superieure de
biotechnologie de Strasbourg, 11, rue Humann, Strasbourg, 67085,
France

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BASE COUNT 166 a 418 c 329 g 223 t
ORIGIN

Query Match      38.6%; Score 878; DB 77; Length 1136;
Best Local Similarity 88.6%; Pred. No. 0.00e+00;
Matches 1007; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

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Db 181 gccgtggggctgctgggcaacgtgtgtcatgttccggcatctccggtacaactaatg 240
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QY 372 TGCAGAGGCTGTGCTCTCCATGACTACTACACATGTTCACATCTTCAACCCCTCACC 431
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RESULT 10
LOCUS SSU71149 686 bp mRNA MAM 02-JAN-1997
DEFINITION Sus scrofa delta opioid receptor mRNA, partial cds.
ACCESSION U71149
NID g1763195
KEYWORDS
SOURCE pig.
ORGANISM Sus scrofa
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euteria; Artiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 686)
AUTHORS Brown,D.R., Poonyachoti,S., Osinski,M.A., Kowalski,T.R.,
Pampusch,M.P., Elde,R.P. and Murtaugh,M.P.
TITLE Delta-opioid receptor mRNA expression and immunohistochemical
localization in porcine small intestine
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 686)
AUTHORS Pampusch,M.P., Osinski,M.A., Brown,D.R. and Murtaugh,M.P.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1996) Veterinary Pathobiology, University of
Minnesota, 1988 Fitch Avenue, St. Paul, MN 55108, USA
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BASE COUNT 117 a 226 c 192 g 151 t
ORIGIN

Query Match      24.3%; Score 552; DB 48; Length 686;
Best Local Similarity 90.2%; Pred. No. 0.00e+00;
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Matches 619; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

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Db	61	ttggcagatgcactgcccacgaacgctgcccctccagagtgccaagtacattgag	120
QY	288	ttggcagatgcactgcccacgaacgctgcccctccagagtgccaagtacattgag	347
Db	121	acctggccttttgggagctgtctctgcaaggccgtactctccatctgactactaca	180
QY	348	acctggccttttgggagctgtctctgcaaggccgtactctccatctgactactaca	407
Db	181	ttcacagcatcttcaacgtccacatgatgagcgctcgaccgtatattgcccgtcgc	240
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QY	888	gaccgcctgt	913

RESULT 11  
LOCUS RATMOP101D 1401 bp mRNA ROD 24-JAN-1994  
DEFINITION Rat mu opioid receptor mRNA, complete cds.

ACCESSION L22455  
NID 9437671

KEYWORDS mu opioid receptor.  
SOURCE Rattus norvegicus (strain Sprague-Dawley) cDNA to mRNA.  
ORGANISM Rattus norvegicus  
Eukaryota; Eutheria; Rodentia; Sciurognathi; Murimorpha; Muridae;

REFERENCE 1 (bases 1 to 1401)  
AUTHORS Thompson,R.C., Mansour,A., Akil,H. and Watson,S.J.  
TITLE Cloning and pharmacological characterization of a rat mu opioid receptor

JOURNAL Neuron 11 (5), 903-913 (1993)  
MEDLINE 94059560  
FEATURES source

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BASE COUNT 330 a 434 c 312 g 325 t  
ORIGIN

Query Match 16.1%; Score 365; DB 91; Length 1401;  
Best Local Similarity 71.9%; Pred. No. 5.32e-282;  
Matches 623; Conservative 0; Mismatches 240; Indels 3; Gaps 2;

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QY	804	gt	863
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BASE COUNT 376 a 479 c 361 g 370 t  
ORIGIN

Query Match 16.1%; Score 365; DB 91; Length 1586;  
Best Local Similarity 71.9%; Pred. No. 5.32e-282;  
Matches 623; Conservative 0; Mismatches 240; Indels 3; Gaps 2;

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RESULT 14  
LOCUS RATMUOR1 2135 bp mRNA ROD 20-OCT-1993  
DEFINITION Rattus norvegicus Mu opiate receptor (MUOR1) mRNA, complete cds.  
ACCESSION L20684  
MID 9409149  
KEYWORDS Mu opiate receptor.  
SOURCE Rattus norvegicus (library: lambda ZAP (Stratagene)) cortex cDNA to mRNA.  
ORGANISM Rattus norvegicus  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;  
Murinae; Rattus.  
REFERENCE 1 (bases 1 to 2135)  
AUTHORS Wang,J.-B., Imai,Y., Epler,M.C., Gregor,P., Spivak,C. and Uhl,G.R.  
TITLE Mu opiate receptor: cDNA cloning and expression  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90, 10230-10234 (1993)  
MEDLINE 94052137  
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BASE COUNT 541 a 590 c 441 g 563 t  
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Best Local Similarity 71.8%; Pred. No. 3.10e-280;  
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QY 264 AACATCTACATCTTCAATCTGGCTTTGGCTGATGCGCTGGCCACGACGAGCTGCCCTTC 323  
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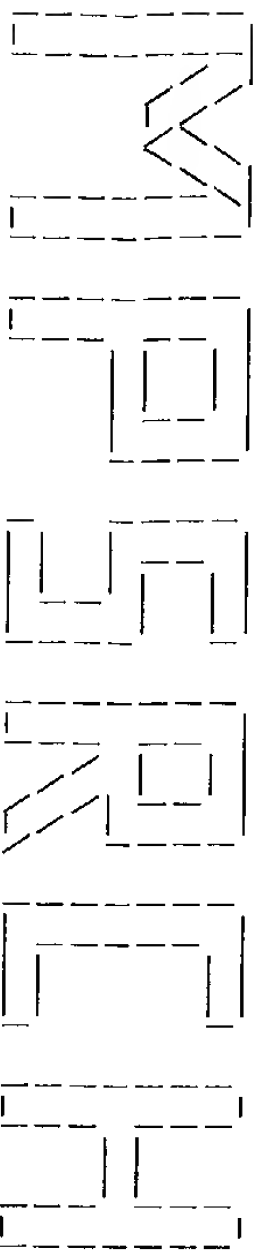


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QY	684	CCGATCCTCATCATCATCACGGTGT	GTATTGGCCCTCATGTCTACTGCCCTGGCCAGCGGTGCGT	743
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DEFINITION	Rat mRNA for rat opioid receptor B, complete cds.			
ACCESSION	D16349			
NID	g391866			
KEYWORDS	G-protein coupled receptor; rat opioid receptors; transmembrane protein.			
SOURCE	Rattus norvegicus (strain Wistar) adult brain cDNA to mRNA, clone PROR15.			
ORGANISM	Rattus norvegicus Eukaryota; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus. 1 (bases 1 to 2397) Fukuda,K., Kato,S., Mori,K., Nishi,M. and Takeshima,H. Primary structures and expression from cDNAs of rat opioid receptor delta- and mu-subtypes FEBS Lett. 327 (3), 311-314 (1993)			
JOURNAL MEDLINE COMMENT	Submitted (03-JUN-1993) to DDBJ by: Hiroshi Takeshima International Institute for Advanced Studies c/o Shimadzu Corporation N-80 1 Nishinokyo-Kuware-hara-cho Kyoto 604 Japan Phone: 075-823-1208 Fax: 075-811-8186. Location/Qualifiers 1.2397 /organism="Rattus norvegicus" 184..1380 /gene="ROR-B" /codon_start=1 /product="rat opioid receptor B" /db_xref="PID:g391867" /translation="MDSSTGPNTSDCDPLAQAASCPAPGSWNLNSHYDGNQSDPCGLNRTGLGNDSLCPQTGSPSMVTAITMALYSIVCVGLFGNELVMYAVRYTKMTATNIIFYNALADALATSTLPFOSVNYLMGTWEFTILCKIVISIDYNNFTSIFTICTMSVDRIYAVCHPVKALDFTRPRNAKIYVNCWWIISSAIGLPMVEMATKYRQSIDCTLTFSHPTWENMLKICVFIFAFIMPVLTVCYGLIMILRLKSVRMLSGSKEDRNLRKITRMVLVVVAIVEIWCWTPIHITYIITALITIIPETTFQTVSWHFCLALGYTNSCLNPV"			
FEATURES	source			
CDS				

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QY	504	GCCAAAGCTGATCATATATATGCACTCTGGGCTTGGCTTCAAGGTGTGCGGGTCCCCATCATG	563	
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Job time : 2151 secs.

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Msrch\_n n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Tue Aug 26 09:48:23 1997; MasPar time 275.82 Seconds  
810.489 Million cell updates/sec  
Tabular output not generated.

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Description: (1-2272) from US08292694A.seq  
Perfect Score: 2272  
N.A. Sequence: 1 CACGCGCGCCCATGAGACTG.....CTTCCACACAACTGTGGCA 2272  
Comp: GTGCGCGCGGTACCTCGAC.....GAAGGTGTGTGACACCCGT

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 134151 seqs, 49196315 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-geneseq27  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 9.769; Variance 5.956; scale 1.640

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2272	100.0	2272	13	Q75927	Mouse delta opioid re	0.00e+00
2	2032	89.4	2216	11	Q66656	Murine delta opioid r	0.00e+00
3	1629	71.7	1821	10	Q56700	Sequence of murine de	0.00e+00
4	365	16.1	1618	14	Q89223	Transcription regulat	9.92e-226
5	365	16.1	1618	14	Q89222	Rat mu opioid recepto	9.92e-226
6	361	15.9	2070	12	Q79199	Rat mu-subtype opioid	5.94e-223
7	351	15.4	1981	10	Q56705	Partial sequence of t	5.19e-216
8	338	14.9	1610	14	Q89226	Human mu opioid recep	5.38e-207
9	336	14.8	2160	15	Q93102	Human mu opiate recep	1.31e-205
10	303	13.3	1142	20	T12550	Human kappa opioid re	8.96e-183
11	291	12.8	1410	13	Q75926	Mouse kappa opioid re	1.73e-174
12	282	12.4	1567	14	Q89233	Rat opioid receptor c	2.79e-168
13	279	12.3	2481	15	Q86725	Mammalian kappa opioi	3.26e-165
14	280	12.3	2706	15	Q92972	Rat opiorph receptor	6.66e-167
15	265	11.7	829	10	Q56703	Partial sequence of t	2.91e-157
16	265	11.7	1330	13	Q75928	Mouse opioid receptor	1.42e-156

c	17	263	11.6	1000	13	Q75931	Human kappa opioid re	3.36e-155
	18	254	11.2	2600	14	Q90096	Mouse kappa-3 opioid	5.15e-149
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	21	105	4.6	1634	7	Q45653	Human somatostatin re	1.31e-48
	22	100	4.4	1518	14	Q83682	Epsilon opioid recept	2.31e-45
	23	98	4.3	1265	7	Q45654	Murine somatostatin r	4.54e-44
	24	92	4.0	1047	2	Q10572	Human Natriuretic pep	3.33e-40
	25	86	3.8	1047	2	Q10572	Human Natriuretic pep	2.29e-36
	26	86	3.8	1110	5	Q29155	Pituitary somatostati	2.29e-36
	27	84	3.7	1054	14	Q83681	Epsilon opioid recept	4.29e-35
	28	81	3.6	1296	7	Q45657	Murine somatostatin re	3.42e-33
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	32	73	3.2	1796	7	Q45658	Murine somatostatin r	3.64e-28
	33	58	2.6	822	5	Q29156	Brain somatostatin re	5.78e-19
	34	52	2.3	1210	15	Q87049	Rat fatty acid bindin	2.15e-15
	35	53	2.3	1254	22	T32033	Proliferation-inhibit	5.54e-16
	36	50	2.2	413	2	Q13400	Mouse U6 intranuclear	3.20e-14
	37	50	2.2	853	9	Q57069	AGE-modified DNA INS-	3.20e-14
	38	50	2.2	13206	1	Q05243	Rat acyl peptide hydr	1.76e-12
	39	47	2.1	2276	14	Q87170	Natural resistance-as	1.76e-12
	40	47	2.1	2294	16	Q92940	Natural resistance-as	1.76e-12
	41	47	2.1	2485	14	Q87167	Natural resistance-as	1.76e-12
	42	47	2.1	3519	16	Q92937	Natural resistance-as	1.76e-12
	43	45	2.0	91	9	Q51746	Oligonucleotide probe	2.46e-11
	44	45	2.0	10614	15	Q89555	Hamster cholesterol 7	2.46e-11
	45	44	1.9	13206	1	Q05243	Rat acyl peptide hydr	9.09e-11

ALIGNMENTS

RESULT 1  
ID Q75927 standard; DNA; 2272 BP.  
AC Q75927;  
DT 17-AUG-1995 (first entry)  
DE Mouse delta opioid receptor MORD1 cDNA.  
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;  
KW transmembrane domain; somatostatin; receptor; human; expression vector;  
KW truncate; chimaeric; assay; probe; ss.  
OS Mus musculus.  
FH Key Location/Qualifiers  
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FT /product= mouse delta opioid receptor  
FT PN WO9428132-A.  
PD 08-DEC-1994.  
PE 20-MAY-1994; U05747.  
PR 20-MAY-1993; US-066296.  
PR 30-JUL-1993; US-100694.  
PR 05-NOV-1993; US-147592.  
PA (ARCH-) ARCH DEV CORP.  
PI Bell GI, Reisine T, Yasuda K;  
DR WPI; 95-022804/03.  
DR P-PSDB; R67670.  
PT Polynucleotides and peptides derived from opioid receptor  
PT polypeptides - for use in therapeutic compositions and in  
PT screening assays for useful drug substances.  
PS Claim 6; Page 215-221; 300pp; English.  
CC The nucleotide sequence of the novel mouse delta opioid receptor gene  
CC MORD1. The gene was isolated from a mouse brain cDNA library using a  
CC fragment (amplified from the cDNA library with primers Q75929-30) as a  
CC probe. The primers are based on the conserved sequences present in the  
CC second and third transmembrane domains of somatostatin (SRI) receptor  
CC subtypes SSTR1, SSTR2 and SSTR3. The 1.3 kb EcoRI-SacI fragment from the  
CC mouse delta opioid receptor clone, lambda msl-2, was subcloned into the  
CC CMV promoter-based expression vector pCMV-6c. The resultant construct  
CC pCMV-msl-2 was transfected into COS-1 cells for protein production. The  
CC gene encoding the opioid receptor can be used to produce complete, the  
CC truncated or chimaeric opioid receptor proteins. The opioid receptors  
CC thus produced are useful for the development of novel assays designed to  
CC select or improve substances, capable of interacting with the opioid

CC receptor proteins, for use in diagnosis, drug design and therapeutic applications.  
Sequence 2272 BP; 485 A; 665 C; 650 G; 472 T;

Query Match 100.0%; Score 2272; DB 13; Length 2272;  
Best Local Similarity 100.0%; Pred.No. 0.00e+00;  
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Db 961 tctaagccttctctgtgacgagaacttcaagcgtgtcttcgcgaagctctgtcgcaagccct 1020

QY 961 TCTAGCCCTTCCCTGAGACGAGAACTTCAAGCGCTGCTCCGCCAGCTCTGTGCGACGCCCT 1020  
Db 1021 gcgcgcgcgaagaacccgcgcagctctccgtcgttccccgcgaagcccaaccagcgtgagcgtg 1080  
|||||  
QY 1021 GCGCGCGCCAGAAGAACCCGCGAGTCTCCGTGCTCCCCGCGCAGGCCAACACGCGGTGAGCCTG 1080  
Db 1081 tcactgcctgcacccccctccgaagycggcgcggtgtgctgcgcctgacctaaccgac 1140  
|||||  
QY 1081 TCACTGCTTGCACCCCCCTCCGACGCGCCCCGGGCGGTGGCGCTGCCCTGACCTACCCGAC 1140  
Db 1141 ctcccccttaaacgcgcctccccaaagtgaagtgtatccagaagccacacagagctccctggy 1200  
|||||  
QY 1141 CTTCCTCTTAACGCCCTCCCAAGTGAAGTGTCCAGAGGCCACACCGAGCTCCCTGGG 1200  
Db 1201 agcgtgtggccaaccaaccaagacagctagaattggyccctgcacaagaaggagccctcgt 1260  
|||||  
QY 1201 AGGCTGTGGCCACACCACAGGACAGCTAGAATTGGGCTTGACAGAGGGGAGGCTCTGT 1260  
Db 1261 gggagcgggycctgaggaatcaaaagctccaggttgaaacggtggygtgaaagacaga 1320  
|||||  
QY 1261 GGGAGCGGGCCCTGAGGAGTCAAAAGCTCCAGGTTGGAACGCTGGGGGTGAGGAAGCAGA 1320  
Db 1321 gctgtgatttcctaactgtatccaattagtaagccctctccaatgggacagagcctccgc 1380  
|||||  
QY 1321 GCTGTGATTTCCCTAAACTGTATTCATTAAGTAAAGCCCTCCCAATGGGACAGAGCCTCCGC 1380  
Db 1381 cttagataacatcgggttctctgcccnaaaagaacacacagctccaagttccaagacccaagga 1440  
|||||  
QY 1381 CTTAGATAACATCGGGTCTGTGCCCAAAAGAACACACAGCTCCAGTCCAAGACCCAAGGA 1440  
Db 1441 ttccagctccaggaacacagaggggtcgatgtattgttgcctgtagagtcaccagcat 1500  
|||||  
QY 1441 TTCCAGCTCCAGGAACCAAGAGGGGTGCGATGATTGTTGGCTGAGAGTCCACGCAATT 1500  
Db 1501 gtgttaaggggaagatctctcatcttagaagaagataaagggacagggcatccaagcaag 1560  
|||||  
QY 1501 GTGTATGGGAGGATCTCTCATCTTAGAGAAAGATAAGGGGACAGGGGCAATTCAGGCCAAG 1560  
Db 1561 caagctggggttgtgtcaggaagataagccccctcccccttggyggygaagataagtgyg 1620  
|||||  
QY 1561 CAGCTTGGGGTTGGTCAAGAGATAAGCCCCCTTCCCTTGGGGGAGGATAAGTGGGG 1620  
Db 1621 gatgtcaacgttggagaagatcaaaagtctcacacaccttctaactactcagctaaac 1680  
|||||  
QY 1621 GATGTCAACGTTGGAGAAGAGTCAAGTCTCACCACTTCTCACTCACTCAAGCTAAAC 1680  
Db 1681 tcgttaggcttagggcaacgttgacttctctgtagagagatatacaagccgggcctgatggy 1740  
|||||  
QY 1681 TCGTTGAGGCTTAGGGCAACGTGACTTCTGTAGAGAGGATACAGCGCGGCTGATGGG 1740  
Db 1741 gcaagctgtgttaatcccaagtcatagtggaagctgagcgtggaanaattaaggaaccaagc 1800  
|||||  
QY 1741 GCAGGCTGTGTAATCCACAGTCATAGTGAGGCTGAGGCTGGAAAATTAAAGAACCAACAGC 1800  
Db 1801 ctgggcaatttagtgtctcaaaataaaatgtaaaagagggctgggaattgtagctcagtgt 1860  
|||||  
QY 1801 CTGGCAATTAGTGTCTCAAAATAAATGTAAAGAGGGCTGGGAATGTAGCTCAGTGTG 1860  
Db 1861 agggtgtttgtgtgagcctctggtgataataaagacaaacaaacaaacaaacaaacaaac 1920  
|||||  
QY 1861 AGGGTGTGTTGTGAGGCTCTGGGATCAATTAAGACAAAACCAACCAACCAAAACCT 1920  
Db 1921 tccaacacacaaacaaacccctcaaacacaaacaaacaaacaaacaaacaaacaaacaaac 1980  
|||||  
QY 1921 TCCAACACACAAACCAACCCCTCAAAACCAAAAACTATGTGGGTGTCTGAGTCTGTT 1980  
Db 1981 tgaagagaacccgcagccctgtatccctgtggygctgttgacagtgggcaagaagcagag 2040  
|||||  
QY 1981 TGAAGAGAACCCGACGCCCTGTATCCCTGTGGGCTGTGGACAGTGGGCAAGCAGAGG 2040  
Db 2041 ctccctgatacctgaaacaaagggcccccaaaagcaagttctaagggagccctgaaaaacgag 2100  
|||||



QY 2041 CTCCTGATCCTGAACAAGGCCCCAAAAGCAAGTTCTAAAGGAGCCCCCTGAACCGAG 2100

Db 2101 taagccttgtgtcaagaagtggagtagaaccagaagaagtgtgctgagtattaaaggca 2160

QY 2101 TAAGCCTTGTGTCAAGAAGTGGAGTAGAACCAGAAGAGTGGCTGAGTGAATTAAGGGCA 2160

Db 2161 cgtgactctcttgcagagagacataggttcgattccacagcaccacacatagtgctcacagc 2220

QY 2161 CGTACTCTCTTGACAGAGACATAGGTTGATTCACAGCACCCACATAGTGGCTCACAGC 2220

Db 2221 catctgtaacccagtcgcagtcacatctaattgcttccaacaactgtggca 2272

QY 2221 CATCTGAACCCAGTCGAGTCAATCTAATGCTTTCCAACAACACTGTGGCA 2272

RESULT 2

ID Q66656 standard; cDNA; 2216 BP.

AC Q66656;

DT 19-JAN-1995 (first entry)

DE Murine delta opioid receptor coding sequence.

KW delta opioid; enkephalin; receptor; mouse; murine; analgesic; pain;

KW drug addiction; neurological disorder; psychiatric; disorder;

KW cardiovascular disorder; ds.

OS Mus musculus.

FM Key Location/Qualifiers

FT CDS 59..1174

FT /\*tag= a

FT /product= opioid\_receptor

PN FR2697850-A.

PD 13-MAY-1994.

PF 10-NOV-1992; 013526.

PR 10-NOV-1992; FR-013526.

PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.

PI Kieffer B;

DR WPI; 94-178255/22.

DR P-PSDB; R66503.

PT New nucleic acid encoding opioid receptor - and related

PT polypeptide, antisense nucleic acid, probes, recombinant cells

PT and ligands, useful in diagnosis and treatment of e.g.

PT neurological disorders

PS Claim 3; Page 16-18; 29pp; French.

CC A cDNA bank constructed from hybridoma NG108-15, was used to

CC transfect COS-1 cells. The cells were tested for ability to bind

CC tritium-labelled Tyr-D-Thr-Gly-Phe-Leu-Thr, in the presence or

CC absence of the opioid antagonist naloxone. Clone K56 was isolated

CC from a positive colony and found to contain a 2216bp insert. This

CC cDNA encodes a delta opioid (enkephalin) receptor with apparent

CC dissociation constant 1.4nM and Bmax 3.9-6.4 pmole/mg protein.

SQ Sequence 2216 BP; 460 A; 647 C; 649 G; 460 T;

Query Match 89.4%; Score 2032; DB 11; Length 2216;

Best Local Similarity 98.8%; Pred. No. 0.00e+00;

Matches 2142; Conservative 0; Mismatches 8; Indels 17; Gaps 7;

Db 51 gcgagcgcatagagctgtgccccttgcccgtgcygagctgcagtcctcgcctcgta 110

QY 4 GCGGCGGCATGGAAGCTGGTGCCCTCTGCCCGTGCGGAGCTGCAAGTCTCTGCCCTCTCA 63

Db 111 accctcgcgaagccttccacagcgcttcccccagcgcgcgcccaatgctcggtgcgc 170

QY 64 ACCCTCTGGAGCGCCTTCCCAAGCGCTTCCCAAGCGGCGGCCCAATGCGTGGGGTCCG 123

Db 171 cgggagcccgtagtgctcctcgccctagccatcgccatcaaccgcgtctactcg 230

QY 124 CGGGAGCCCGTAGTGCTCTGCTCCCTCGCCCTAGCCATCGCCATCAACCGCGCTCTACTCG 183

Db 231 ctgtgtgcgcagtggtggtctctggcaacgtgctcgtcatgtttggcatcgtccggtaca 290

QY 184 CTGTGTGCGCAGTGGGCTCTGTGGCAACGTGCTCGTCATGTTGGCATCGTCCGGTACA 243

Db 291 ccaaatgaagaccgccaacacatctacatcttcaatctggtttggtgatgctggtg 350

QY 244 CCAAAATTGAAGACCGCCACCAACATCTACATCTTCAATCTGGCTTTGGCTGATGGCTGG 303

Db 351 ccaccagcagctgcocctccagagcgcccaagtacttgatggaacgtggccgtttggcg 410

QY 304 CCACCAGCAGCGCTGCCCTTCCAGAGCGGCCAAGTACTTGATGGAACGTGGCCGTTGGCG 363

Db 411 agctgctgtgaaggtctgtctctccattgactactacaacatgttcaactagcatctca 470

QY 364 AGTGCTGTGCAAGGCTGTGCTCTCCATTGACTACTACAAACATGTTCACTAAGCATCTTCA 423

Db 471 ccctcaacatgatagcggtgagaccgctacattgtctgtccatccgttcaagccctgg 530

QY 424 CCCTCACCATGATGAGCGGTGAGCCGCTACATTGCTGTCTGCCATCTCTCAAGCCCTGG 483

Db 531 actccggaaccaagccaagcgctgatacatatatatgcatctggttcttgcttcag 590

QY 484 ACTTCGGACACCAACCAAGGCCCAAGCTGATCAATATATGCACTGTGGTCTTGAG 543

Db 591 gtgtcggtgtcccatcatcatgtcatgtgcaagtgaac-aaccccggtatgtgcaagtgtat 649

QY 544 GTGTGGGGTCCCCATCATGTGTCATGGCAGTGAACCAACCCCGGATGTGCAAGTGTAT 603

Db 650 gcatgttccagttccccaagtcac-agctgtgactgg-aacatgtgaaccaagatctgcgtgt 707

QY 604 GCATGCTCCAGTTCCCAAGTCCCAAGCTGGTACTGGGACACTGTGACCAAGATCTGGCGTGT 663

Db 708 tcctcttgccttcgtgtgtgcccgaatccatcatcatcaacggtgtgctatgacctatgctac 767

QY 664 TCCTCTTTCGCTTGTGTGTGGCCGATCTCATCATCAGGTGTGTATGGCTCATGTCTAC 723

Db 768 tgcgccttgagcagcgtgctgtctgtccggttccaagagagaagaccgcagcctgcgcg 827

QY 724 TGGCCTGGGCAAGCGTGCCTGTGCTGTCCGGTTCCAAAGAGAGAGACCGCAGCCTGCGGC 783

Db 828 gcatcagcgcatgtgtgctgtgtgtgtggcgccctcgtgtgtgtgctggtgcccacatcc 887

QY 784 GCATCACGGGCATGTGTGTGTGTGGTGGCGCCTTCTGTGTGTGTGGCGCCATCC 843

Db 888 acatcttcgtcatcgtctgtgacgctgtgtgacatcatcgcgcgcacccactgtgtgtg 947

QY 844 ACATCTTGTCAATCGTCTGGACGCTGTGTGACATCAATCGCGCGACCCACTTGTGTGTG 903

Db 948 ccgcactgcaacctgtgcatgctgctgtggctacgccaacagagccctcaaccggttctct 1007

QY 904 CCGGACTGCAACCTGTGCAATGCGGTGGGCTACGCCAACAGACAGCCTCAACCCGGTCTCT 963

Db 1008 acgccttcctgagcagaacttcaagcgtgcttccgcgcagctctgtgcagccctgcg 1067

QY 964 ACGCCTTCTTGACGAGAACTTCAAGCGCTGCTTCCGCCAGCTCTGTGCAGGCCCTGGCG 1023

Db 1068 gccgcgaagaaccgcgcagctctcgtcgtcccccgcgaagccaaccagcgtgagcgttca 1127

QY 1024 GCCGCCAAGAACCCGGCAGTCTCCGTCTCCGCCGCAAGGCCACACGCGTGAGCGGTACA 1083

Db 1128 ctgcttgcaacccctccgacggtcccggtggtgtggtgctgcccgtgaacctaacccgaactt 1187

QY 1084 CTGCCAGACCCCTCCGACGGCCCGGGCGGTGGCGCTGCCCTGACCTACCCGACCTT 1143

Db 1188 ccccttaaacgccccctcccaagtgaagtgtatccaagagccaacacagagctccctgggaag 1247

QY 1144 CCCCTTAAACGCCCTTCCCAAGTGAAGTATCCAGAGGGCCACACCGAGCTCCCTGGGAGG 1203

Db 1248 ctgtggccaaccaaccaagagctagaatttggccttgcaacagagggagcgctcgttggg 1307

QY 1204 CTGTGGCCACCAACGAGAGAGCTAGAATTGGGCTGCACAGAGGGGAGGCTCTCTGTGGG 1263

Db 1308 gaacgggcttgaggtatcaaaagctccaggttggaacgttgggttgaagacagagct 1367

QY 1264 GACGGGGCCTTGAGGATCAAGGCTCCAGGTTGGAACGgtgggggtGAGGAAGCAGAGCT 1323

Db 1368 ggtgattcctaactgtatcaattagtaagccctcacaattgggaacagagcctccgctt 1427

QY 1324 GGTGATTCTTAACCTGTATCCATTAGTAAGGCCCTCTCCAATGGGACAGAGCCTCCGCTT 1383

Db	1428	gaagataacatcggggttctctgcccctttttgaacaccccaagctccagtcccaagaccgaagatt	1487
QY	1384	GAGATAACATCGGGTTC	1442
Db	1488	ccagctccaggaacccaggagggcagtgatgaggggtcgatgattgtgttcgtgaagtc	1547
QY	1443	CCAGCTCCAGGAACCA	1491
Db	1548	ccagcattgtgttatatgsggagatctctcatcttagaagaataagsggacaggcatt	1607
QY	1492	CCAGCATTTGTGTTATG	1551
Db	1608	cagcgcaagcgacgttggggttgtgtcagggagataagcccccttccttggsgggagga	1667
QY	1552	CAGGCAAGCGACGCTT	1611
Db	1668	taagtggggatgtgtcaacgtttggagaaggtccaagtctcaccaccttctcaactact	1727
QY	1612	TAAAGTGGGGATGTG	1671
Db	1728	cagctaaactcgttgaaggctagggccaaagtgacttctctgttagagagatacaagccgg	1787
QY	1672	CAGCTAAACTCGTTG	1730
Db	1788	ggcctgatgggcaagggcctgtgttaatcccagtcatagtggaagctgaggtgsgaaattaa	1847
QY	1731	GCCTGATGGGGCAAGC	1789
Db	1848	ggaccaacagccttgggcaatttagtgtctcaaaataaaatgtaaagagggctgggaattgt	1907
QY	1790	GGACCAACAGCCTGGG	1849
Db	1908	agctcagtggtaggggttgtgtgtgaggtcctgtggatcaataagacaacaacccaacca	1967
QY	1850	AGCTCAGTGTAGGGT	1909
Db	1968	acccaaaacccctccaaacaacaacccaacccctcaaaccaaaaaactatgtgtggtgtctc	2027
QY	1910	ACCAAAAACCTTCCAA	1969
Db	2028	cgagctgtgttgaagaaaccccgagccctgtatccctgttggsgctgttgacagtggc	2087
QY	1970	TGAGTCTGTTTGAAGA	2029
Db	2088	agaagcagaggtccctgtgatactgaacaagggccccaagaagcaagttctaagsgaaccc	2147
QY	2030	AGAAACAGAGGCTCC	2089
Db	2148	ctgaacaccgagtaagccttgtgtcaagaagtgggagtracaaccagaagaagtggctgagt	2207
QY	2090	CTGAACACCGAGTAAG	2149
Db	2208	gctttag 2214	
QY	2150	GATTAAAG 2156	
RESULT 3			
ID	Q56700	standard; cDNA; 1821 BP.	
AC	Q56700;		
DT	15-SEP-1994	(first entry)	
DE	Sequence of murine delta opioid receptor in the DOR-1 cDNA clone.		
KW	Opioid receptor; morphine; opiate; ss.		
OS	Mus musculus.		
FX	KEY	Location/Qualifiers	
FT	CDS	29.1139	
FT	/*tag= a		
PN	WO9404552-A.		
PD	03-MAR-1994.		
PF	13-AUG-1993; U07665.		
PR	13-AUG-1992; US-929200.		
PA	(REGC ) UNIV CALIFORNIA.		
PI	Edwards RH, Evans CJ, Kaufman D, Keith DE;		

DR	MPI; 94-083099/10.
DR	P-PsDB; R48629.
PT	DNA encoding opioid receptors and antibodies against this
PT	receptor - used to express and locate these receptors, and screen
PT	cnds. for opioid (ant)agonist activity
PS	Claim 1; Fig 5; 74pp; English.
CC	A CDNA library was constructed using mRNA isolated from the NG109-15
CC	cell line. A single clone, named the DOR-1 clone was isolated.
CC	Comparisons with known sequences in Genbank showed highest homology
CC	between DOR-1 and the G-protein-coupled somatostatin receptor. Other
CC	features of the DOR-1 clone AA sequence deduced from the cDNA
CC	sequence include 3 consensus glycosylation sites at residues 18 and
CC	33 (predicted to be in the extracellular N-terminal domain), and at
CC	residue 310 (close to the C-terminus and predicted to be
CC	intracellular). Phosphokinase C consensus sites are present within
CC	predicted intracellular domains, at residues 242,255, 344 & 352.
CC	Seven putative membrane-spanning regions were identified. The DOR-1
CC	clone produces a delta receptor with a predicted mol. wt. of 40,558
CC	kaltions prior to post-translational modifications.
SQ	Sequence 1821 BP; 339 A; 559 C; 541 G; 382 T;
Query Match 71.7%; Score 1629; DB 10; Length 1821;	
Best Local Similarity 98.2%; Pred. No. 0.00e+00;	
Matches 1781; Conservative 0; Mismatches 8; Indels 24; Gaps 13;	
Db	21 gcgcgcatgagctgtgcccctcctgcacctgccccgtgcggagtgcagtcctcgccctcgca 80
QY	4 GCGGCGCATGAGCTGGTGCCCTCTGCCCGTGGGAGCTGCAGTCCTCGCCCCTCCTCA 63
Db	81 accctcgcagcgccttccacgcgccttcccacgcgcgcgcgcgaatgcctgcgggtcgc 140
QY	64 ACCTCTCGAGACGCTTTCCACAGCGCCTTCCCCAGCGCGGGGCCAATGCGTGGGGTGC 123
Db	141 cggagaccctagtgcctcgtccctgcacctagccatgccataccgcgctctactcgg 200
QY	124 CGGAGCCCGTAGTGCCTCTCCTCGCCCTAGCCATCGCCATCACCGCGCTTACTTGG 183
Db	201 ctgtgtgcgcagtggggtctcttgaggcaacgtgctgcatagtttggcatcgtccgtaca 260
QY	184 CTGTGTGCGCAGTGGGGCTTCTGGGCAACGTGCTGTCATGTTTGGCATCGTCCGGTACA 243
Db	261 ccaaattgaagaccgcacacaacatctacatcttcaatctgcttggctgatgcgtg 320
QY	244 CCAAATTGAAGACC GCCAACATCTACATCTTCAATCTGGCTTGGCTGATGGCTGG 303
Db	321 ccaccagcacgctgcacctcccaagagcgccaagtactgatgaaacgtggccgtttggcg 380
QY	304 CCACCAGCACGCTGCCCTTCCAGAGCGCCAAGTACTTGATGGAACGTGGCCGTTTGGCG 363
Db	381 agctgtctgcaagcgtgtgctctccattgtaactactacaacatgttcaactagcatcttca 440
QY	364 AGCTGCTGTGCAAGGCTGTGCTCTCCATTGACTACTACACATGTTCACTAGCATCTTCA 423
Db	441 cccctacccatgatgagcgttggaacccgtacacattgtcgtctgcacatccctgtcaaacccctgg 500
QY	424 CCCTCACCATGATGAGCGGTGGACCGCTACATTTGCTGTGCCATCCTGTCAAAGCCCTGG 483
Db	501 acttccggaacacacgacgaagccaaagctgatcaatatatgatcatctgygtcttgcttcaag 560
QY	484 ACTTCCGGACACCAAGCCAAAGCTGATCAATAATATGCACTTGGGCTTGGCTTCAG 543
Db	561 gtgtcggggtccccaatcatgtgcatgtagcagtaaccaacccccgggatgtgtcagtgat 620
QY	544 GTGTGGGGGTCCCATCATGCTCATGGCAGTGAACCAACCCGGGATGTTGCAGTGTTAT 603
Db	621 gcatgtccacgttccccaggtccacgctgtgactgggacacatgtgaaccaagatctgcgtt 680
QY	604 GCATGCTCCAGTTCCTCCAGTCCAGCTGTGTACTGGGACACTGTGACCAAGATCTGCGTGT 663
Db	681 tctctttgoccttgcgtgtgcgataloatcatcatcaacgtytgtatgagccatagtctac 740
QY	664 TCCTCTTTGGCCTTGTGTGTGGCGATCCTCATCATCAACGGTGTGCTATGGCCTCATGTCTAC 723

Db	741	tgcgctgcgcagcagctgtgcgtctgtccggttccaagygagaagacgcgacctgcgc	800
QY	724	TGGCGCTGCGCAGCGGTGCCTGTGCTGCCGTCCAGAGAGAAGACCGCACTGCGGC	783
Db	801	gcatacgcgcgatgtgtcgtgtgtgttggtggcgcccttcgtgtgtctgtggccccatcc	860
QY	784	GCAATCAGCGCGCATGGTGTGCTGGTGTTGGCGGCTTCGTGTGTGTCTGGCGCCATCC	843
Db	861	acaatttcgtcatcgtctgyagcctgtgtgaacatcaatcgcgcgaccacttgtgtgtg	920
QY	844	ACAATTCTGTCATCGTCTGGACCGTGTGGACATCAATCGCGGGAACCACTTGTGTGG	903
Db	921	ccgcactgcacctgtgcatatgcygtggtgctaagccaacagcacgcacctcaacccggttcct	980
QY	904	CCGCACTGCACCTGTGCATTTGGCGTGGCTAACGCCAACAAGCACAGCCTCAACCCGGTCTCT	963
Db	981	aagccttcctgtgacgcagaacttcaaagcgtctgtcttcgcgacgtctgtcgcacgccctgcg	1040
QY	964	AAGCCTTCTCTGGACGAGAACTTCAAGCGCTGCTTCGGCCAGCTCTGTGCACGCCCTTGGC	1023
Db	1041	gccgcaccaagaacccggcagttccgtcgtcccccgaagccaacaaacgcgttagcgtgtca	1100
QY	1024	GCCGCCAAGAACC CGG CAG TCTCC GTCC GCG CCAG GCC AACC AGCG TGAG CGTGTCA	1083
Db	1101	ctgccttgcacccctccgcagcgcgcgcggcggtgtgcgtcgtcgcgcctgaacctaccgcacct	1160
QY	1084	CTGCCTGCACCCCTCCGACGCGCCCCGGCGGTGGCGCTGCCGCTGAACCTAACCCGACCTT	1143
Db	1161	cccccttaacgcgccctcccgaagtgaagtga--cagaggcacacaccgaagctccctggtagg	1218
QY	1144	CCCCCTTAACGCCCCCTCCCAAGTGAAGTATCCAGAGGCCACACCGAGCTCCCTGGGAGG	1203
Db	1219	ctgtgycacacccacagagacagctagaatttggccctgcacagaggggagccctcgttggg	1278
QY	1204	CTGTGGCCACCAACCAGGACGACTGAATTGGCCCTGCACAGAGGGGAGGCCCTCCTGTGGG	1263
Db	1279	gaacgg--cctlagggatcaaaaagcgtccaaggttgaacgftggggggtfyagaaagcagagct	1336
QY	1264	GACGGGGCCTGAGGGATCAAAGGCTCCAGGTTGGAACGGTGGGGGTGAGGAAGCAGAGCT	1323
Db	1337	ggtgattccctaactgtatccattagtaagggcctct--aatgggacagagcctccgcctt	1394
QY	1324	GGTGATTCCCTAAACTGTATCCATTAGTAAGGCCCTCTCCAATGGGACAGAGCCTCCGCTTT	1383
Db	1395	gagataaacatcggtgttccttggcccttttgaacacccagctccagtlccaagacccaagatt	1454
QY	1384	GAGATAACATCGGGTCTGCCCCAAAAGAACACC-AGCTCCAGTCCCAAGACCCCAAGGATT	1442
Db	1455	ccagctccaaaaccagagaggggcagtgatgggtgcgatgattgtgttgctgagagtrcc	1514
QY	1443	CCAGCTCCA-----GGAAC--CAG-GA-GGGGTGATGATTGTGCTTGAGAGTCCC	1493
Db	1515	agcaatttgttatgtgggaggtatctctcatctcttagagaaga--aggggacagggcatlca	1572
QY	1494	AGCATTTGTGTTATGGGGAGGATCTCTCATCTTAGAAGATAAGGGGACAGGGCATTTCA	1553
Db	1573	ggcaaggcagcttgggtttgtgtcaggagataaagcccccttcctltggggggagagata	1632
QY	1554	GGCAAGGCAGCTTGGGTTTGGTCAAGAGATAAGCGCCCCCTTCCTTGGGGGAGGATA	1613
Db	1633	agtgggggatgt--acgttggagaagagtcaaaagtctcaccacacttctaactactca	1690
QY	1614	AGTGGGGATGTCAACGTTGGAAGAAGTCAAAGTTTCAACCACTTCTAACTACTCA	1673
Db	1691	gctaactcgttggagctaggggccaaacgttgacctctctgttagagag--tacaaagccgggc	1748
QY	1674	GCTAAACTCGTTGAGGCTAGGGC-AACGTGACTTCTCTGTAGAGAGGATTACAAGCCGGGC	1732
Db	1749	ctgatggggcaggcctgtgttaatcccaagtcatagtggaagcctgaagctgynaatatgaag	1808
QY	1733	CTGATGGGGCAGGC-TGTGTAATCCCAAGTCATAGTGAAGGCTGAGGCTGAAAAATTAAAG	1791
Db	1809	accaacagccccg 1821	

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QY      1792 ACCACAGCCTGG 1804
|||||
RESULT  4
ID      Q89223 standard; cDNA; 1618 BP.
AC      Q89223;
DT      20-OCT-1995 (first entry)
DE      Transcription regulatory protein cDNA.
KW      Mu opioid receptor; MOR-1; gene therapy; diagnostic;
KW      transcription regulatory protein; ss.
OS      Rattus sp.
FH      Key
FT      CDS                      Location/Qualifiers
FT      CDS                      339..1235
FT      /*tag= a
PN      W09507983-A.
PD      23-MAR-1995.
PF      13-SEP-1994; U10358.
PR      13-SEP-1993; US-120601.
PA      (INDV ) UNIV INDIANA FOUND.
PI      Yu L;
DR      WPI; 95-131351/17.
DR      P-PSDB; R71965.
PT      New nucleic acid encoding new human mu opioid receptor - and
PT      related vectors, transformed cells, antibodies etc., useful in
PT      diagnosis, treatment and drug screening.
PS      Disclosure; Page 199-203; 266pp; English.
PS      A 365 bp fragment of the mouse delta opioid receptor was used to
CC      screen a rat brain cDNA library under low stringency conditions.
CC      One positive clone included the sequence given in Q89222, encoding a
CC      mu opioid receptor, MOR-1 (R71964). Sequence analysis revealed an
CC      alternative reading frame (Q89223) encoding a zinc
CC      finger-containing transcription regulatory protein (R71965).
SQ      Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T;

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	Query Match	16.18;	Score 365;	DB 14;	Length 1618;
	Best Local Similarity	71.98;	Pred. No. 9.92e-226;		
	Matches	623;	Conservative	0;	Mismatches 240; Indels 3; Gaps 2;
Db	403	tccatggtcacagcaccattacacatcatgcccctctactctatctgcgtgtgtgtagtggccctc	462		
QY	144	TCCCTCGCCCTAGGCCATTCGCCATCACCGCGCTCCTACCTGGCTGTGTGCGCAGTGGGGCTT	203		
Db	463	ttcggaaccttcctgtgcatgtatgttatgttaagatataccaaaaatgaagactgccacc	522		
QY	204	CTGGGCACACGTGCTCGTCATGTTTGCCATCGTCCGGTACACCAAATTGAAGACCGCCACC	263		
Db	523	aacatctacatttccaaccttgctctgycagagcccttagcgaccagtataactggccctt	582		
QY	264	AACATCTACATCTTCAATCTGGCTTTGGCTGATGGCTGGCCACCAAGCAGCGTGCCTTC	323		
Db	583	cagaagtgtcaactacctgatgygaaacatggcccttcogaaacaacacctctgcaagatcgtg	642		
QY	324	CAGAAGCCCAAGTACTTGATGGAACGTGGCCGTTTGCGAGCTGTGTGCAAGGCTGTG	383		
Db	643	atctcaatagattactacaacaatglttacccaggcataattcaacctctgcaacatgagcgtg	702		
QY	384	CTCTCATTTGACTACTACAACATGTTCACTAGCATCTTCAACCTCAACCATGATGAGCGTG	443		
Db	703	gaccgctacattgctgtctgcccaccagtcgaagccctggtatttccgtataccccccgaaat	762		
QY	444	GACCGTACATTGTGTCTGCCATCTCTGCAAGCCCCGTGAACTTCCGGACACCAAGCCAAG	503		
Db	763	gccaaaaatcgtcaaacgtctgcaactgfatccctctcttctgccaatcggtctgctgtaaty	822		
QY	504	GCCAAAGCTGATCATATATATGCACTCTGGGCTTGGCTTCAGGTGTGGGGTCCCACATCATG	563		
Db	823	ttcatggaacaccaaataacaggcaggggtccatagattgcaacctcaacyttctccac	882		
QY	564	GTCATGGCAGTAGAACCAACCCCGGATGGTCAGTGTATGCAATGCTCCAGTTCCCCAGT	623		
Db	883	ccaacctgttactgggagaaacctgctcaaatctgttcttatctcttgcgttcatcatg	942		



QY 624 CCCAGCTGCTACTGGGACACTGTGACCAAGATCTGGCTGTCTCTTTGCCCTTCGTGTG 683  
Db 943 ccgatacctacatcaactgtgtgttaacggcctgatgatcttaacgactcaagagcgttcgc 1002  
QY 684 CCGATCCTCATCATCACGGGTGTGCTATGGCCCTCATGTACTGCGCCTGGCGAGCGTGGCT 743  
Db 1003 atgctatcgggctccaaagaagagacaggaatctgcgcagagatcacccggatgtgtctg 1062  
QY 744 CTGCTGTCCGGTTCCAAGAGAGAGACCGCAGCCTGCGGCGCATTCACGCGCATGTGCTG 803  
Db 1063 ctgtgcgtggtgtattattatcgtctgcctggaccccccatccacatctaactcatcaaa 1122  
QY 804 GTGGTGGTGGGGCGCCTTCGTGTGTGCTGGGGCCCATCCACATCTTCGTCACTGCTCTGG 863  
Db 1123 ccgctgatac-acg--attccagaacacacatttcagaccglttccttgccacttcgtcatt 1179  
QY 864 ACGCTGTGGACATCAATCGGCCGACCCACTTGTGTGGTGGCCGACATGCACCTGTGCATT 923  
Db 1180 gcttggggttacacgaaacagctgcctggaatccagttcctttaagccttcctggaataaac 1239  
QY 924 GCGCTGGGCTACGCCAACAGCAGCCTCAACCCGGTTCTCTACGCTTCTCTGGACGAGAAC 983  
Db 1240 ttcaagcgatgcttcaagagattctg 1265  
QY 984 TTCAAGCGCTGTCTCCGCCAGCTCTG 1009

RESULT 5  
ID Q89222 standard; cDNA; 1618 BP.  
AC Q89222;  
DT 20-OCT-1995 (first entry)  
DE Rat mu opioid receptor cDNA.  
KW Mu opioid receptor; MOR-1; gene therapy; diagnostic; ss.  
OS Rattus sp.  
FH Key Location/Qualifiers  
FT CDS 214..1410  
FT /\*tag= a  
PN WO9507983-A.  
PD 23-MAR-1995.  
PF 13-SEP-1994; U10358.  
PR 13-SEP-1993; US-120601.  
PA (INDV ) UNIV INDIANA FOUND.  
PI Yu L;  
DR WPI; 95-131351/17.  
DR P-PSDB; R71964.  
PT New nucleic acid encoding new human mu opioid receptor - and  
PT related vectors, transformed cells, antibodies etc., useful in  
PT diagnosis, treatment and drug screening.  
PS Disclosure; Page 190-194; 266pp; English.  
CC A 365 bp fragment of the mouse delta opioid receptor was used to  
CC screen a rat brain cDNA library under low stringency conditions.  
CC One positive clone included the sequence given in Q89222, encoding a  
CC mu opioid receptor, MOR-1 (R71964). MOR-1 was stably expressed in  
CC transfected CHO cells.  
SQ Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T;

Query Match 16.1%; Score 365; DB 14; Length 1618;  
Best Local Similarity 71.9%; Pred. No. 9.92e-226;  
Matches 623; Conservative 0; Mismatches 240; Indels 3; Gaps 2;

Db 403 tccatggtcacagccattaccatcatgscctctactctatcgtgtgtgtagtggcctc 462  
QY 144 TCCCTGCGCCCTAGCCATCGCCATCACCGCGCTCTACTCGGCTGTGTGGCAGTGGGCTT 203  
Db 463 ttcggaacttcctgtgtcatgtatgtatgttaagatacaccaaaatgaagactgcacac 522  
QY 204 CTGGGCAACGTGCTGTCATGTTGGCATCGTCCGGGTACACCAAAATTGAAGACCGCCACC 263  
Db 523 aacatctacattttcaaocttgctctgacagacgccttagcagccagtracactgcocctt 582  
QY 264 AACATCTACATCTCAATCTGGCTTTGGCTGTGATGCGCTGGCCACCAAGCAGCTGCCCTTC 323  
Db 583 cagagtgtcaactactgatggaacatgagcccttcggaaccatcctctcgcaagatcgtg 642

QY 324 CAGAGCGCCAAAGTACTTGATGGAAACGTGGCCGTTTGGCGAGCTGTGTGAAGGCTGTG 383  
Db 643 atctcaatagattactacaacatggttcaccagcatattcaaccctctgcaccatgagcgtg 702  
QY 384 CTCTCCATTGACTACTACACATGTTCACTAGCATCTTCACCCCTCAACCATGATGAGCGTG 443  
Db 703 gaccgctacattgtctgtctgcacccagtcacaaagccctggaatttcgtaacccccgaat 762  
QY 444 GACCGCTACATTGCTGTCTGCCATCTCTCAAAAGCCCTGGACTTCGGACACACAGCCCAAG 503  
Db 763 gccaaaaatcgtcaacgctcgaactggaatcctctctctgcacatcgtctgcctgtaatg 822  
QY 504 GCCAAGCTGATCAATATAIGCATCTGGGTCTTGCTTCAAGTGTGGGGTCCCATCATG 563  
Db 823 ttcatggaaccacaataacaggaagggtccatagattgaacctcaacgtctccac 882  
QY 564 GTCATGGCAGTGACCCCAACCCGGGATGGTGAGTGGTATGCATGCTCCAGTTCCCAGT 623  
Db 883 ccaacctggtactgagagaaactgctcaaatctgtcttattcttcgcttcatcatg 942  
QY 624 CCCAGCTGTACTGGGACACTGTGACCAAGATCTGCGTGTCTCTTGGCTTCGTGTG 683  
Db 943 ccgatacctacatcaactgtgtgttaacggcctgatgatcttaacgactcaagagcgttcgc 1002  
QY 684 CCGATCCTCATCATCACGGGTGTGCTATGGCCCTCATGTACTGCGCCTGGCAGCGTGGCT 743  
Db 1003 atgctatcgggctccaaagaagagacaggaatctgcgcagagatcaacccggatgtgtctg 1062  
QY 744 CTGCTGTCCGGTTCCAAGAGAGAGACCGCAGCCTGCGGCGCATTCACGCGCATGTGCTG 803  
Db 1063 gtgtgcgtggtgtattattatcgtctgcctggaaccccccatccacatctaactcatcaaaa 1122  
QY 804 GTGGTGGTGGGGCGCCTTCGTGTGTGCTGGGGCCCATTCACATCTTCGTATGCTCTGG 863  
Db 1123 gcgctgatac-acg--attccagaacacacatttcagaccglttccttgccacttcgtcatt 1179  
QY 864 ACGCTGTGTGACATCAATCGGCCGACCCCACTTGTGTGGTGGCCGACATGCACCTGTGCATT 923  
Db 1180 gcttggggttacacgaaacagctgcctggaatccagttcctttaagccttcctggaataaac 1239  
QY 924 GCGCTGGGCTACGCCAACAGCAGCCTCAACCCGGTTCTCTACGCTTCTCTGGACGAGAAC 983  
Db 1240 ttcaagcgatgcttcaagagattctg 1265  
QY 984 TTCAAGCGCTGTCTCCGCCAGCTCTG 1009

RESULT 6  
ID Q79199 standard; cDNA; 2070 BP.  
AC Q79199;  
DT 19-APR-1995 (first entry)  
DE Rat mu-subtype opioid receptor cDNA.  
KW Mu-subtype opioid receptor; MSOR; drug addiction; ds.  
OS Rattus rattus.  
FH Key Location/Qualifiers  
FT CDS 83..1154  
FT /\*tag= a  
FT /product= Mu-subtype\_opioid\_receptor  
PN EP-612845-A.  
PD 31-AUG-1994.  
PF 09-FEB-1994; 101968.  
PR 26-FEB-1993; US-026140.  
PA (AMCY ) AMERICAN CYANAMID CO.  
PI Corbett MJ, Eppler CM, Shieh H, Zysk JR;  
DR WPI; 94-265963/33.  
DR P-PSDB; R65188.  
PT pure mu-type opioid receptor protein - and nucleic acid coding

PT for it  
PS Claim 1; Fig 11; 39pp; English.  
CC R65188 is the rat mu-subtype opioid receptor protein purified  
CC from rat brain membranes, with biotinyl-b-endorphin (R56666)  
CC as its ligand. It is encoded by the nucleotide sequence Q79199





[illegible]

	RESULT	6
ID	Q89226	standard; cDNA; 1610 BP.
AC	Q89226;	
DT	20-OCT-1995	(first entry)
DE	Human mu opioid receptor cDNA.	
KW	Mu opioid receptor; MOR; gene therapy; diagnostic; ss.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	CDS	239..1441
FT	/*tag=	a
PN	W09507983-A.	
PD	23-MAR-1995.	
PE	13-SEP-1994; U10358.	
PR	13-SEP-1993; US-120601.	
PA	(INDV ) UNIV INDIANA FOUND.	
PI	Yu L;	
DR	WPI; 95-131351/17.	
DR	P-PSDB; R71966.	
PT	New nucleic acid encoding new human mu opioid receptor - and	
PT	related vectors, transformed cells, antibodies etc., useful in	
PT	diagnosis, treatment and drug screening.	
PS	Claim 5; Page 208-210; 266pp; English.	
CC	A cDNA library constructed from human caudate nucleus mRNA was	
CC	screened with rat mu opioid receptor cDNA under conditions of	
CC	low stringency. One positive clone included the sequence given in	
CC	Q89226, encoding a mu opioid receptor MOR (R71964). The cDNA	
CC	is used for prodn. of recombinant MOR, in gene therapy, etc.	
CC	Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T;	

Query Match	14.98;	Score 338;	DB 14;	Length 1610;
Best Local Similarity	70.68;	Pred. No. 5.38e-207;		
Matches 604;	Conservative 0;	Mismatches 248;	Indels 3;	Gaps 3;

Db	446	gccatcacgatacatgcccccttaactccatcgtgtgtcgtgtgtggggtctcttcggaacttc	505
QY	156	gccatcggccatcacccggctcttactcggctctgtgtggcagatggggcttctgggcaacgtg	215
Db	506	ctgtgtcatgtatgtgatctgtcaagatacacccaagatgaaagctgtccaccaacatctacatt	565
QY	216	ctcgtcatgtttggcatcgtccgggtacccaattgaagaccggccaccacaactctacatc	275
Db	566	tccaacctgtctctggcagatgccttagccaaccagtaacctgcccctccagaagtgtgaat	625
QY	276	ttcaatctggcctttggctgatggcctggccaccagcacgctggcccttcagagggccaag	335
Db	626	taactaatgggaacatgycgcaattctggaaccatcccttgcagaatagtgtatcccatagat	685
QY	336	tacttgatggaaacgtggccgtttggcgaagctgctgtgcaaggctgtgctctccatttgac	395
Db	686	tactataacatgttcaccaccagcatatccaacctctgcaccatgtagtgttgatcogatacaatt	745
QY	396	tactacacaacatgttcactactagcatcttccacctcaaccatgatgagcgctggaacggctacatt	455
Db	746	gcagctctgcacccctgtccaagcccttagatttccgtactccccggaatgccaanaattatc	805
QY	456	gctgtctgccatccctgtccaaggcccttggaacttccggacaaccagccaaaggcccaactgcatc	515

Db	806	aatgtctgcaactggaatccctctctcttcaggccattggtctctccgtlaaagtltcatggtctaca	865
QY	516	AAATATATGCACTGGGCTCTGGCTTCAGGTTGCGGGTCCCCCATCATGTCTCATATGGCAGTG	575
Db	866	acaaatacacgagcaagttccatagattgtacactaacaattctctcatccacaacctggtac	925
QY	576	ACCCAAACCCGGGATGGTGTGACATGGTATGTCATGCTCCAGTTCCCCAGTCCCAAGCTTGGTAC	635
Db	926	tgggaaaaacctgctgaagatctgtgtttcatctctgcacctcaattatgccaagtgctcatc	985
QY	636	TGGGACACTGTGACCAAGATCTGCGTGTCTCTTTCCTCTTTGCCCTTCGTGGTGGCGAATCCTCATC	695
Db	986	attaccgtgtgtctatbgacatgatatcttgcgcctcaagaagtgtccgcatagtctctcgtgc	1045
QY	696	ATCACGGTGTGTATAGCCCTCATGCTACTCTGCGCCTGCGCAGCGTGGCTGTCTGCTGTCCGGT	755
Db	1046	tccaaagaaaagagacaggaatcttcgaagyalccaccagatggtgctggtgtggt	1105
QY	756	TCCAAGAGAGAAGGACCGCAGCCTGCGCGCATCAGCGCATGTGCTGTGCTGTGCTGTGGGC	815
Db	1106	gtgttcacgtctgtcgtgactcccatcattacaattacgtcatcatattaagcctgtgttaca	1165
QY	816	GCCTTCGTGTGTGCTGGGCGCCCATCCACATCTTCGTATCGTGTGAACCTGTGTGAC	875
Db	1166	atccca-gaaactacgttccagac-tgttt-cttggcaactctcgtcatctgctctaggttac	1222
QY	876	ATCAATCGGCGGACCCACCATTTGTGTGTGGCCGACACTGCACCTGTGCATTGGCGTGGGCTAC	935
Db	1223	acaaacagctgcctcaaccccaagtccttatatgcatlctctgatatgaanaactcaaacgatatgc	1282
QY	936	GCCACACAGCAGCCTCAACCCGGTCTCTACGCGCTTCCTGTGACGAGAGACTCAAGCGCTGC	995
Db	1283	ttcagagagttctgt 1297	
QY	996	TTCCGCCACGCTCTGT 1010	

	RESULT	9
ID	Q93102	standard; cDNA; 2160 BP.
AC	Q93102:	
DT	11-DEC-1995	(first entry)
DE	Human mu opiate receptor cDNA.	
KW	Mu opiate receptor; hMOR; opiate agonist; opiate antagonist; drug abuse; analgesic; ds.	
KW		
OS	Homo sapiens.	

	Key	Location/Qualifiers
FH	CDS	213..1415
FT		

PN WO9520667-A1.  
PD 03-AUG-1995.  
PF 30-JAN-1995; U01144.  
PR 28-JAN-1994; US-188275.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (USSH ) US SEC DEPT HEALTH.  
PI Johnson PS, Persico AM, Uhl G, Wang J;  
DR WPI: 95-275452/36.  
DR P-PSDB; R76780.  
PT New DNA encoding human mu opiate receptor - used esp. for screening  
PT cpds. for activity as opiate agonists or antagonists  
PS Claim 4; Page 24-25; 49pp; English.  
CC hMOR cDNA was obtd. from a human cerebral cortical cDNA library  
CC screened with fragments of a rat mu opiate receptor. Cloned hMOR  
CC DNA can be used as probes to examine the structure and function of  
CC hMOR genes or to screen individuals for susceptibility to drug  
CC abuse. Expression in e.g. COS cells allows production of  
CC recombinant hMOR1.  
SQ Sequence 2160 BP; 563 A; 566 C; 455 G; 576 T;

Query Match	14.8%;	Score 336;	DB 15;	Length 2160;
Best Local Similarity	70.5%;	Pred. No. 1.31e-205;		
Matches 603;	Conservative	0;	Mismatches 249;	Indels 3; Gaps 3;

[illegible]

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RESULT      10
ID          T12550 standard; cDNA; 1142 BP.
AC          T12550;
DT          03-SEP-1996 (first entry)
DE          Human kappa opioid receptor cDNA.
KW          Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
KW          neurology; diagnosis; ds.
OS          Homo sapiens.
FH          Key
FT          CDS
FT          CDS
FT          /tag= a
FT          /product= kappa_opioid_receptor

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FT /note="incomplete termination codon"  
PN WO9601898-A1.  
PD 25-JAN-1996.  
PF 07-JUL-1995; F00912.  
PR 11-JUL-1994; FR-008531.  
PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.  
PI Kieffer B, Simonin F;  
DR WPI; 96-097628/10.  
PT P-PSDB; R88722.  
PT New nucleic acid encoding the human Kappa opioid receptor - useful  
PT in diagnosis and therapy, and for isolating receptor ligands and  
PT modulators  
PS Claim 3; Page 13-15; 30pp; French.  
CC This sequence codes for the human Kappa opioid receptor and was  
CC obtained from two overlapping cDNA fragments isolated from a  
CC human placental cDNA library. The fragments were amplified from  
CC the library using PCR primers based on the sequence of human  
CC genomic clones which hybridised with a murine delta receptor cDNA  
CC probe. Nucleotide probes derived from the kappa opioid receptor  
CC coding sequence are useful for diagnosis of neurological, cardio-  
CC vascular and psychiatric disorders associated with opioid  
CC receptors.  
SQ Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T;

Query Match	13.3%;	Score 303;	DB 20;	Length 1142;
Best Local Similarity	70.7%;	Pred. No. 8,96e-183;		
Matches 619;	Conservative	0;	Mismatches 244;	Indels 12; Gaps 9;
Db 163	tcceccggccatcccggtcatcatcacagcggtctactccgtagtgttcgtggttg	222		
QY 144	TCCTTCGCCCTTAGCCATCGCCATCACCGCGCTCTACTCGGCTGTGTGGCAGTGGGCTT	203		
Db 223	gtgggcaactcgctggtcatgttctgtatcatccgatacaacaagatgaagacagcaacc	282		
QY 204	CTGGGCAACGTGCTCGTCATGTTTGGCATCGTCCGGGTACACCAAAATTGAAGACCGCCACC	263		
Db 283	aacattacatatattaacctgctttggcagatgctttagttactacaacctatgccctt	342		
QY 264	AACATCTACATCTTCATCTGGCTTTGGCTGATGGCGTGGCCACACGACGCTGCCCTTC	323		
Db 343	cagagtacggtctacttgatgaattccctggcctlttggggatgtgtctgtgcaagatgta	402		
QY 324	CAGAGCGCCAAGTACTTGATGGAAACGTGGCCGTTTGGGAGCTGTGTGCAAGGCTGTG	383		
Db 403	attcccatgtattactacaacaatgtttcaaccagcatcttcaaccttgaaatgtagcgtg	462		
QY 384	CTCTCCATTGACTACTACACACATGTTCACTAGCATCTTCAACCTCACCATGATGAGCGTG	443		
Db 463	gaaccgctacattgccgtgtgcccaccccggtgaagcgtttgacctccgcacacacctgaag	522		
QY 444	GACCGCTACATTGCTGTCTGGCCATCCTGTGCAAAAGCCCTGGACTTCGGACACGCCAAG	503		
Db 523	gcaaaagatcaataatctgtcatctggtcgtctgtcgtcatcgttggcatctctgcaata	582		
QY 504	GCCAAAGCTGATCAATATATGCACTGTGGTCTTTGGCTTCAGGTGTCCGGGTCCCATCATG	563		
Db 583	gtcccttgagggaccaaagtcagggaagacgtcgtatgtcatgtagtgctcccttgcaagtc	642		
QY 564	GTCATGGCAGTGACCCCAACCCCGGGAATGGTGCAGTGGT-ATGCA-TGCTCC---AGTTC	617		
Db 643	ccaagatgactactccctgtgtgggaccccttcatgaagatctgcgtcttcatctttgcc	702		
QY 618	CCC-A-G-TCCAGCTGGTACTGGGACACTGTGACCAAGATCTGCCTGTTCCTTTGGCC	674		
Db 703	ttcgtgatccctgtcctcatcatcatcgtctgtctacacccctgatgatcctcgtctcaag	762		
QY 675	TTCTGTGTGCGGATCTCTCATCATCACGCTGTGCTATTGGCCTCATGTACTGGGCTTGCGC	734		
Db 763	agcgtccggctccttctctgctcccgagagaagaagatcgcaacctgcgttagatcaaccaga	822		
QY 735	AGCGTGGCTGTGCTGTCCGGTTCACAAGGAAGAACCGCAGCCTGCGGGCCATCACGGCGC	794		
Db 823	ctggtcctggtgtgtgtggcagcttcctcgtcgtcgtgactcccatcaataattcatc	882		



QY 795 ATGTTGCTGGTGGTGGTGGCGCCCTTCGTGGTGGTGGCGCCCATCCACATCTTCGTC 854  
Db 883 ctggtggagctctggygagcaccctccacagc-acag-ctgctctctccagctatt-ac 939  
QY 855 ATCGTCTGGACGCTGGTGGACATCAATCGGCGGACCCCACTTGTGGTGGCCGCACTGCAC 914  
Db 940 ttctgcacgccttaggctatataccacagtagcctgaatcccatctcttaagccttctt 999  
QY 915 CTGTGCATTGGCGCTGGGCTACGCGCAACAGACGCTCAACCCGGTCTCTACGCCCTTCCTG 974  
Db 1000 gatatgaacttcaagcggtgtttccgggacttctg 1034  
QY 975 GACGAGAACTTCAAGCGCTGCTTCGCCCACTCTG 1009

RESULT 11.  
ID Q75926 standard; DNA; 1410 BP.  
AC Q75926;  
DE Mouse kappa opioid receptor MOR1 cDNA.  
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;  
KW transmembrane domain; somatostatin; receptor; human; expression vector;  
KW truncate; chimaeric; assay; probe; ss.  
OS Mus musculus.  
FH Key location/Qualifiers  
FT CDS 186..1328  
FT /\*tag= a  
FT /product= mouse kappa opioid receptor  
PN W09428132-A.  
PD 08-DEC-1994.  
PE 20-MAY-1994; U05747.  
PR 20-MAY-1993; US-066296.  
PR 30-JUL-1993; US-100694.  
PR 05-NOV-1993; US-147592.  
PA (ARCH-) ARCH DEV CORP.  
PI Bell GI, Reisine T, Yasuda K;  
DR WPI; 95-022804/03.  
DR P-PSDB; R67669.  
PT Polynucleotides and peptides derived from opioid receptor  
PT polypeptides - for use in therapeutic compositions and in  
PT screening assays for useful drug substances.  
PS Claim 10; Page 207-211; 300pp; English.  
CC The nucleotide sequence of the novel mouse kappa opioid receptor gene  
CC MOR1. The gene was isolated from a mouse brain cDNA library using a  
CC fragment (amplified from the cDNA library with primers Q75929-30) as a  
CC probe. The primers are based on the conserved sequences present in the  
CC second and third transmembrane domains of somatostatin (SRIF) receptor  
CC subtypes STR1, STR2 and STR3. The 1.2 kb PstI fragment from the mouse  
CC kappa opioid receptor clone, lambda msl-1, was subcloned into the CMV  
CC promoter-based expression vector pCMV-6b. The resultant construct  
CC pCMV-msl-1 was transfected into COS-1 cells for protein production. The  
CC gene encoding the opioid receptor can be used to produce complete,  
CC truncated or chimaeric opioid receptor proteins. The opioid receptors  
CC thus produced are useful for the development of novel assays designed to  
CC select or improve substances, capable of interacting with the opioid  
CC receptor proteins, for use in diagnosis, drug design and therapeutic  
CC applications.  
SQ Sequence 1410 BP; 322 A; 360 C; 337 G; 391 T;

Query Match 12.8%; Score 291; DB 13; Length 1410;  
Best Local Similarity 70.8%; Pred. No. 1.73e-174;  
Matches 597; Conservative 0; Mismatches 234; Indels 12; Gaps 8;

Db 368 catcacgcgtgtctactctgtgtatttgggtggtggttagtggcgaattctctgtcat 427  
QY 164 CATCACCGCGCTCTACTCGGCTGTGTGGCAGTGGGGCTTCTGGGCAACGTGCTCGTCAT 223  
Db 428 gttgtcatcatcgcgatatacagaagatgaagaccgcaaccaacatcatataatcaact 487  
QY 224 GTTTGGCATCGTCCGGTACACCAAAATTAAGACCGCCACCAACATCTTCAATCT 283  
Db 488 ggctttggcagatgcttggttactaccataatgcccttccagagtgtgtctacttgat 547

QY 284 GGCTTTGGCTGATGCGCTGGCCACCAACGACGCTGCCCTTCCAGAGCCCAAGTACTTGAT 343  
Db 548 gaattcttgsccttlttgagatggtctatgcaagattgtcatattccattgactactaaca 607  
QY 344 GGAACGTTGGCCGTTTGGCGAGCTGCTGTGCAAGGCTGTGCTTCCATTGACTACTACA 403  
Db 608 catgtttaacagcatattacaccttgaccatgatgatgagtgtggaacgcctacattgtgtg 667  
QY 404 CATGTCTACTAGCATCTTCAACCCCTCAACCATGATGAGCGGTGGACCGCTTACATTTGCTGTG 463  
Db 668 ccacctgtgaaagccttggacttccgaacaccttgaagaagaagatcatcaacatctg 727  
QY 464 CCATCCTGTCAAAAGCCCTGGACTTCCGGACACCAAGCCAAAGCTGATCAATATATG 523  
Db 728 cattggctcctgycatcatctgttgtatatacagcgatagtccttggagcaccaaagt 787  
QY 524 CATCTGGGTCTTGGCTTCAGGTGTGGGGTCCCCATCATGTGTCATGGCAGTGACCCAAC 583  
Db 788 cagggaagatgtgatgtcatgtgaatgctctccttgcagttccctgatgatataatctctg 847  
QY 584 CCGGATGGTGCAGTGGT-AT-GCATGTCC---AGTTCCCAAGTCCACAGCTGTACTG 637  
Db 848 gtgggarcctctcatgaagatctgtctctgtctgtcttgccttgtgatcccaagtcctcat 907  
QY 638 G-GACA-CTGTG-ACCAAGATCTGGGTCTTCTCTTTCCTTCGTGTGTCGGATCCCTCAT 694  
Db 908 catcatgtctgtctacacacctgtatctcctgcgcctgaagagtgtccgctcctgtctgtg 967  
QY 695 CATCACGGTGTGCTATGCGCTCATGTCTACTGCGCCTGCGCAGCGGTGCTGTGTCGG 754  
Db 968 ctcccgagagaagagcgaatctcccgccgcatcaccaagctgtgtgtagtgtgtgc 1027  
QY 755 TTCCAAGAGAAGGAGCAGCCGACGCTGGCGGCATCACGGCGCATGTGTTGTTGGG 814  
Db 1028 agtcttcacatctgttggacccccattacatcttlatcctgtt--ggaagctctgga 1085  
QY 815 CGCCTTCGTGGTGTGCTGGGGCGCCCATCCACATCTTCGTCACTGTGTGACGCTGTGGA 874  
Db 1086 -agcactccacagcacagcgtgccctctccagctattatttctgtattgcttggtta 1144  
QY 875 CATCAATCGGCGCGACCCCACTTGTGGTGGCGGACACTGCACCTGTGCATTGGCGTGA 934  
Db 1145 taccacagcagcctgaatcctgttctctatgaccttcttgatgaanaactcaagcgtgt 1204  
QY 935 CGCCACAGCAGCCTCAACCCGGTCTCTACGCCCTTCTTGAGAGAGAACTCAAGCGCTG 994  
Db 1205 tt 1207  
QY 995 CTT 997

RESULT 12  
ID Q89233 standard; cDNA; 1567 BP.  
AC Q89233;  
DE 20-OCT-1995 (first entry)  
DE Rat opioid receptor cDNA.  
KW Opioid receptor; MOR-1; gene therapy; diagnostic; ss.  
OS Rattus sp.  
FH Key location/Qualifiers  
FT CDS 173..1276  
FT /\*tag= a  
FT W09507983-A.  
PN W09507983-A.  
PD 23-MAR-1995.  
PE 13-SEP-1994; U10358.  
PR 13-SEP-1993; US-120601.  
PA (INDV ) UNIV INDIANA FOUND.  
PI Yu L;  
DR WPI; 95-131351/17.  
DR P-PSDB; R71968.  
PT New nucleic acid encoding new human mu opioid receptor - and  
PT related vectors, transformed cells, antibodies etc., useful in  
PT diagnosis, treatment and drug screening.



PS Example 9; Page 218-222; 266bp; English.  
CC The cDNA given in Q89233 was isolated from a rat brain library by  
CC low stringency hybridization with rat mu opioid receptor cDNA  
CC (Q89222). The clone encoded a 367-amino acid protein (R71968)  
CC that showed high homology with mu, kappa and delta opioid receptors  
CC but lacked affinity for their ligands, suggesting it to be  
CC a novel member of the opioid receptor family.  
SQ Sequence 1567 BP; 313 A; 440 C; 402 G; 412 T;

Query Match 12.4%; Score 282; DB 14; Length 1567;  
Best Local Similarity 68.0%; Pred. No. 2.79e-168;  
Matches 579; Conservative 0; Mismatches 267; Indels 5; Gaps 5;

Db 318 tcaccatcgtgggctctacttgctgtgtgcatcgggggtccctggggaactgcctcg 377  
QY 160 TCGCCATCACCGCGCTCTACTCGGCTGTGTGGCAGTGGGCTTGTGGCAACGTGCTCG 219  
Db 378 tcatgtatgtcatcctcagggcacacccaagatgaagacagctaccacattacatat 437  
QY 220 TCATGTTGGCATCGTCCGGTACACCAATGAAGACCGCCACCAACATCTACATCTTCA 279  
Db 438 atctggcactggtctataccctggtcttgtaacactgcccctccaggcacagacatcc 497  
QY 280 ATCTGGCTTGGCTGATGCGCTGGCCACGACGCTGCCCTTCCAGAGCCCAAGTACT 339  
Db 498 tactggcttcctggccatttgggaatgcaactctgcaagactgtcatctatcgactact 557  
QY 340 TGATGGAACGCTGGCGCTTTGGCGAGCTGCTGTGCAAGGCTGTGCTTCCATTGACTACT 399  
Db 558 acaacatgtttaccagcaacttttactctgacccgcatgagcgttagaccgctatgtgcta 617  
QY 400 ACAACATGTTCATAGCATCTTCACCCCTCACCATGATGAGCGGTGACCGCTACATTGCTG 459  
Db 618 tctgccaccctataccgtgccccttgatgttcgaaacatccagcaaaagccagcgtgtt-aat 676  
QY 460 TCTGCCATCTCTGTCAAAGCCCTGGACTTCCGGACA-CCAGCCAAAGCCCAAGCTGATCAAT 518  
Db 677 gtggccatatggggccctggctcagtgtgtgtgttccctgttgccatcatggttcagca 736  
QY 519 ATATGCATCTGGGCTTGGCTTCAAGTGTGGGGTCCCCATCATGGTCAATGGCAAGTACC 578  
Db 737 caagtggaaagtgaagagatcgagtgtcgtgtgagatccctgcccctcaggaactattgg 796  
QY 579 CAACCCCGGGATGGTGCAGTGTGATGCATGCTCCAGTCCCAAGTCCCAAGCTGGTACTGG 638  
Db 797 ggcctgtatttcgcaatctgcatcttcccttttcccttcatacctcctgtgtcatc 856  
QY 639 GACACTGTGACCAAGATCTGCGTGTCTTGGCTTCCGCTTCCGTAATCTCATCATC 698  
Db 857 tctgtctgtctacagcctcatgatctgacagactcgtgtgtccgtctgcttccaggtcc 916  
QY 699 ACGGTGTGTATGGCTCTCATGCTACTGCGCTGGCGAGCGTGGCTGTCTGTCGGTTCC 758  
Db 917 cgggagaaggaccgaaacctggcggtatatacctcgactgtgtcgtgtgtgtgtgtgtg 976  
QY 759 AAGGAGAAGGACCGGACGCTGCGCGCATCAACGCGCATGGTGTGTGTGTGGGCGCC 818  
Db 977 ttgtgggctgtcgtggaagcctgtgcaagtggttgtcctgtt-tcaagagactg-gtgtttc 1034  
QY 819 TTCTGTGTGTGTGGGCGCCCATCAACATCTTGTGATCGTGTGGAACGCTGTGTGACATC 878  
Db 1035 agccaggtagtgtagact-gcagttgcatcctcgtcgcttctgcaagccctggtgtatgtc 1093  
QY 879 AATCGCGCGACCCACTTGTGGTGGCGGCACTGCACCTGTGCATTTGGCTGGGCTACGCC 938  
Db 1094 aacagttgtcacaatcccatctctatagtcttccctgtgatgagaacttcaagcctgctt 1153  
QY 939 AACAGCAGCCCTCAACCCGGTCTCTAAGCCTTCCCTGGACGAGAACTTCAAGCGCTGCTTC 998  
Db 1154 agaaagtctctg 1164  
QY 999 CGCCAGCTCTG 1009

RESULT 13  
ID Q86725 standard; cDNA; 2481 BP.  
AC Q86725;  
DE 01-DEC-1995 (first entry)  
DE Mammalian kappa opioid receptor protein cDNA.  
KW Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic;  
KW amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.  
OS Rattus rattus.  
FH Key Location/Qualifiers  
FT CDS 111..1253

FT /product= kappa opioid receptor  
PN J07070191-A.  
PD 14-MAR-1995.  
PE 30-JUL-1993; 190261.  
PR 09-JUL-1993; JP-170591.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
DR WPI; 95-144857/19.  
DR P-PSDB; R72591.  
PI kappa opioid receptor protein and cells expressing it - useful  
PI for the screening of compounds for analgesic and hypnotic  
PI properties  
PS Claim 2; Page 9-10; 15pp; Japanese.

CC The nucleotide sequence of the novel mammalian kappa opioid receptor  
CC cDNA. The gene was isolated by amplifying a fragment from rat brain mRNA  
CC by reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from  
CC the mouse delta-opioid receptor gene. This fragment was cloned into the  
CC plasmid pCRIT to produce pR11. The plasmid pR11 was used to probe a rat  
CC brain DNA library in lambda ZAP1 to obtain a clone of the rat kappa  
CC opioid receptor gene, designated pROPR2. This clone was introduced into  
CC E.coli JM109 for production of the receptor protein. The receptor protein  
CC is useful for screening of analgesic and hypnotic compounds including  
CC peptides and proteins.  
SQ Sequence 2481 BP; 629 A; 588 C; 544 G; 720 T;

Query Match 12.3%; Score 279; DB 15; Length 2481;  
Best Local Similarity 70.1%; Pred. No. 3.26e-166;  
Matches 591; Conservative 0; Mismatches 240; Indels 12; Gaps 8;

Db 293 catcacgcgtctactctgtgtgtgttgtgtgtggttagtgggcaattccctgtcat 352  
QY 164 CATCACCGCGCTCTACTCGGCTGTGTGGCGCAGTGGGGCTTCTGGCCAAAGTGTCTCAT 223  
Db 353 gtttgcatactccgatacaccaagatgaagaccgcaaccacatctacatatlaacct 412  
QY 224 GTTGGCATCGTCCGGTACACCAATTAAGACCGCCACCAACATCTACATCTTCAATCT 283  
Db 413 ggccttggcagatgcttgggttactaccactatggcccttccagagtgctgtcacttgat 472  
QY 284 GGCCTTGGCTGATGCGCTGGCCACCAACGAGCTGCCCTTCCAGAGCGCCAAAGTACTTGAT 343  
Db 473 gaattctggccttbtggagatgttctgtgcaagattgtcaatttccattgactactaca 532  
QY 344 GGAACGTGGCGGTTTGGCGAGCTGTGCAAGGCTGTGTCTCCATTGACTACTACAA 403  
Db 533 catgtttaccagcatattcaccttgaccatgatgagtgtggaaccgctacattgcccgtgtg 592  
QY 404 CATGTCACTAGCATCTTACCCCTCACCATGATGAGCGGTGACCGCTACATTGTCTGTG 463  
Db 593 ccaccctgtgaagccttggatttccgaacaccttgaagaagcaagatcatcaacatctg 652  
QY 464 CCATCTCTGTCAAAGCCCTGGACTTCCGGACACCAAGCCCAAGCTGATCAATATATG 523  
Db 653 catttggctactgcatcatcgttgtgtatatcagcgtatgtccttggagaccacaagt 712  
QY 524 CATCTGGGCTCTTGGCTTCAAGTGTGCGGGTCCCCATCATGCTCATGAGTGAACCAACC 583  
Db 713 cagggaagatgtgtgatgtcaatgtcctccttgcaattcctgatgatgaatatctctg 772  
QY 584 CCGGATGTGTGAGTGGT-AT-GCATGCTCC---AGTTCCCAAGTCCAGCTGTACTG 637  
Db 773 gtgggacctcttcatgaagatctgttctcgtcttgccttgttatccctgtctaat 832

QY 638 G-GACAC-TGAG-ACCAAGATCTGGGTGTCTCTTGGCCTTCGTGGTGGCCGATCCTCAT 694  
Db 833 catcaattgtctgtctaacacccctgatgatccctgcgttgaaagatgtccgcgtctctctcggg 892  
QY 695 CATCACGGGTGTGCTATGGCCTCATGTCTACTGCGCCTGGCCAGCGGTGGCTGTCCGG 754  
Db 893 ctctcgagagaaggaagccgaatatctccgcggagatcaccaagctgtgtctgtgtagtgttc 952  
QY 755 TTCCAAGGAGAAGGACCGCAGCCTGGCGGCATCACGGCATGTGCTGTGTGTGGTGGG 814  
Db 953 agtcttcaatactgttggaccccatcacatcttatacctgttc--gaagctctagg- 1009  
QY 815 CGCCTTGTGTGTGCTGGCGCCCATCACATCTTCGTCACTGCTGGACGCTGGTGA 874  
Db 1010 cagcacctctcacagcacagctgtctctctctagtattacttctgcattgccttggtta 1069  
QY 875 CATCAATCGGGCGACCCCACTTGTGTGGCGGCACTGCACCTGTGCATTGGCGTGGGCTA 934  
Db 1070 taccacagcagcttgatccctgttctctatgccttctctgtatgaaactcaagcggtg 1129  
QY 935 CGCCAACAGCAGCCTCAACCCGGTCTCTACGCCCTTCCTGGACGAGAAGCTCAAGCGCTG 994  
Db 1130 ttt 1132  
QY 995 CTT 997

RESULT 14

ID Q92972 standard; DNA: 2706 BP.  
AC Q92972;  
DT 22-DEC-1995 (first entry)  
DE Rat opiorph receptor OR7 DNA.  
KW Opiorph receptor; opioid; ss.  
OS Rattus sp.  
PN WO9519986-A1.  
PD 27-JUL-1995.  
PF 20-JAN-1995; U00939.  
PR 21-JAN-1994; US-185360.  
PA (AMCY ) AMERICAN CYANAMID CO.  
PI Eppler CM, Hulmes JD, Ozenberger BA;  
DR WPI; 95-269412/35.  
DR P-PSDB: R76638.  
PT New isolated DNA encoding an opiorph receptor - used to develop  
PT prods. for identifying opioid agonists and antagonists and for  
PT detection and manipulation  
PS Disclosure; Fig.1; 35PP; English.  
CC Primers based on rodent opioid receptors were used to amplify rat  
CC genomic DNA. Products were re-amplified and subcloned into pCR-II  
CC vector and amplified in E. coli. Plasmid DNAs were isolated, and  
CC an unspliced sequence was obt'd. (Q92972) encoding the transmembrane  
CC domain opiorph receptor protein OR7.  
SQ Sequence 2706 BP; 569 A; 675 C; 704 G; 758 T;

Query Match 12.3%; Score 280; DB 15; Length 2706;  
Best local Similarity 67.9%; Pred. No. 6.66e-167;  
Matches 578; Conservative 0; Mismatches 268; Indels 5; Gaps 5;

Db 252 toaccatcgtgggctctacttggctgtgtgcatcggggggtcctcctgggaaactgcctcg 311  
QY 160 TCGCCATCACCGCGCTCTACTCGGGTGTGTGGCAGTGGGGCTTCTGGGCAAGTGTCTG 219  
Db 312 tcaatgtatcatcctcagcacaccaagaatgaagacagctacacaacattacataatta 371  
QY 220 TCATGTTGGCATGCTCCGGTACACCAAAATTGAAGACCGCCACCAACATCTACATCTTCA 279  
Db 372 atctggcactgctgatataccctgtctgtctaactgcgctccagggcacagacatcc 431  
QY 280 ATCTGGCTTTGGCTATGCGCTGGCCACACGACGCTGCCCTTCAGAGCGGCAAGTACT 339  
Db 432 tactggcttctgcgaatttgggaatgatgcacttcgcaagactgtcaattgtctatcgact 491  
QY 340 TGATGAAACGTGGCCGCTTTGGCGAGCTGCTGTGCAAGGCTGTGCTCTCCATTGACTACT 399

Db 492 acaacatgtttaccagcacttttactctctgaaccgccatgagcgttagaccgctatgtgtcta 551  
QY 400 ACAACATGTTCACTAGCATCTTCACCCCTCACCATGATGAGCGGTGACCCGTACATGTGCTG 459  
Db 552 tctgccaccctatccgtgcccttgatgttcggacatccagcaagcccaagctgtt-aat 610  
QY 460 TCTGCCATCTCTGTCAAAGCCCTGGACTTCCGGACA-CCAGCCAAAGGCCAAGCTGATCAAT 518  
Db 611 gtggccaatatgggcccttgctcagtggttgtgttctcctgttgcacatcatggttcagca 670  
QY 519 ATATGCATCTGGGCTCTTGGCTTCAGGTGTGGGGGTCCCATCATGATGTCATGGCAGTGACC 578  
Db 671 caagtgaagatgaagagatcgaagtgcgtgtgagatccctgcctcctcaggaactatgg 730  
QY 579 CAACCCCGGAGTGGTGCAGTGATGCATGCTCCAGTTCCAGTCCCAAGTCCAGCTGTTACTGG 638  
Db 731 ggcctgtattcgcatctgcatacttcccttttcccttcatacctcctgtgtatcatc 790  
QY 639 GACACTGTGACCAAGATCTGCGTGTTCCTCTTGCCTTGTGTGGTGGCCGATCCTCATCATC 698  
Db 791 tctgtctgtacagcctcatgatctgaagactcgtgtgtctcgtctcgttcaagctcc 850  
QY 699 ACGGTGTGCTATGGCCTCATGCTACTGCGCCTGGCAGCGGTGCTGTGCTGTCCGTTCC 758  
Db 851 cgggagaaggaaccgaaacctgcgcgtatacctcgcactgctgtcgtgtagtgtgctgtg 910  
QY 759 AAGGAGAAGAGACCGCAGCCTGCGGGCGCATCAGCGCATGTGCTGTGTGTGGGCGCC 818  
Db 911 ttgtggcctgtcgtgagcctgtgcaggtgttgtcctgtt-tcaaggaactg-gtgttcc 968  
QY 819 TTCGTGTGTGTGTGGCGCCCATCCACATCTTGTCTATGCTGTGACGCTGTGTGACATC 878  
Db 969 agccagtagtagact-gcaagtgccatccctgcgtctctgcacagccctgggtatgtc 1027  
QY 879 AATGGCGCGACCCCACTTGTGTGGTGGCGCACTGCACCTGTGCATTGGCTGTGGCTACGCC 938  
Db 1028 aacagttgtcaatcccatctctatgctttcctgtgatgagaactcaagcctgttt 1087  
QY 939 AACAGCAGCCTCAACCCGGTCTCTACGCTTCTTGACGAGAGAAGTCAAGCGCTGCTTC 998  
Db 1088 agnaagtctg 1098  
QY 999 CGCCAGCTCTG 1009

RESULT 15

ID Q56703 standard; DNA: 829 BP.  
AC Q56703;  
DT 15-SEP-1994 (first entry)  
DE Partial sequence of the human mu opioid receptor  
DE genomic clone H20 (MORA).  
KW Opioid receptor; morphine; opiate; ss.  
OS Homo sapiens.  
PN WO9404552-A.  
PD 03-MAR-1994.  
PF 13-AUG-1993; U07665.  
PR 13-AUG-1992; US-929200.  
PA (REGC ) UNIV CALIFORNIA.  
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;  
DR WPI; 94-083099/10.  
PT DNA encoding opioid receptors and antibodies against this  
PT receptor - used to express and locate these receptors, and screen  
PT cpds. for opioid (ant)agonist activity  
PS Example; Fig 8c; 74pp; English.  
CC To isolate opiate receptor genomic clones, 300,000 human genomic  
CC clones and a similar number of mouse genomic clones were probed  
CC with the 1.1 kb mouse delta opioid receptor clone DOR-1 Pst/XbaI  
CC fragment. One mouse clone and three human genomic clones were  
CC isolated. The 3 human clones had very different EcoRI patterns  
CC which indicated that three different genes were represented by the  
CC human genomic clones which were designated H3, H14 and H20. H20 maps  
CC to chromosome 6. It encodes the human mu receptor. In addition, H20

CC appears to contain a CACACA marker (Q56704) which provides a means  
 CC to track the inheritance of this gene.  
 SQ Sequence 829 BP; 182 A; 205 C; 134 G; 214 T;

Query Match 11.7%; Score 266; DB 10; Length 829;  
 Best Local Similarity 62.8%; Pred. No. 2.91e-157;  
 Matches 484; Conservative 0; Mismatches 282; Indels 5; Gaps 5;

```

Db 18  tacaccaagatgaagactgcccacacacatctacatttcaacctgtctg-caagatgoc 76
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 240  TACACCAAATTGAAGACGGCCACCAACATCTACATCTTCAATCTGGCTTGGCTGATGCC 299

Db 77  ttagccaccagtaacctgcccctccagagtgtagaattacctaattggaacatggccattt 136
    |  |||||  ||  |||||  |||||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
QY 300  CTGGCCACACGACGCTGCCCTTCCAGAGCGCCAGTACTTGATGGAACGTGGCCGTTT 359

Db 137 ggaaccatcccttgcaagatagtgatctccatagattactataacatgttccaccagcata 196
    ||  ||  |||||  ||  |||||  ||  |||||  ||  |||||  |||||  |||||
QY 360  GGCAGAGCTGCTGTGCAAGGCTGTGCTCTCCATGTGACTACTACACATGTTCACCTAGCATC 419

Db 197 ttacccctctgcaccatgagtgttgatcgatacatgtcagtcgcacccctgtcaaggcc 256
    |||||  ||  |||||  ||  |||||  ||  ||  |||||  |||||  |||||  |||||
QY 420  TTCACCCCTCACCATGATGAGCGGTGAGCCGCTACATTGCTGTGCCATCCTGTCAAAAGCC 479

Db 257 ttagatttccgtactcecnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 316
    ||  |||||  ||  ||
QY 480  CTGGACTTCCGGACACCAAGCCAAAGGCTGATCAATATATGCACTGGGCTTTGGCT 539

Db 317 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 376
QY 540  TCAGGTGTCGGGGTCCCATCATGTGTCATGGCAGTAGCCCAACCCCGGATGGTGCAGTG 599

Db 377 gattgtacactaacattctctcaccacctgtaactggaanaacctgtcgaagatctgt 436
    ||  ||  ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 600  GTATGCATGCTCCAGTTCCTCCAGTCCAGCTGTGTAAGTGGACACTGTGACCAAGACTCTGC 659

Db 437 gtttcatctctgccttcattatagccagtgctcatcaatcaaccgtgtgtcattgactgatg 496
    ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 660  GTGTTCCTCTTGGCTTCGTGTTGGTGGCCGATCCATCATCAGGGTGTGCTATGGCCCTCATG 719

Db 497 atcttgccctcaagagtgtcgcgcatgctctcgtgctccaaagaaaggaaggaatctt 556
    ||  |||||  ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 720  CTACTGGCCCTGCGCAGCGGTGCTGTGCTGTCCGCTTCCAAGGAGGAGGACCGCAGCCTG 779

Db 557 cgaaggaatcaccagaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 616
    ||  |||||  ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 780  CGGCGCATCAGCGCATGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 839

Db 617 attcacattacgtatcatcaataaagccttggttaaatccca-gaaactagttccagac 675
    ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 840  ATCCACATCTTCTGTCATGCTGTGACGCTGTGTGACATCAATCGGCGGACCCACTTGTG 899

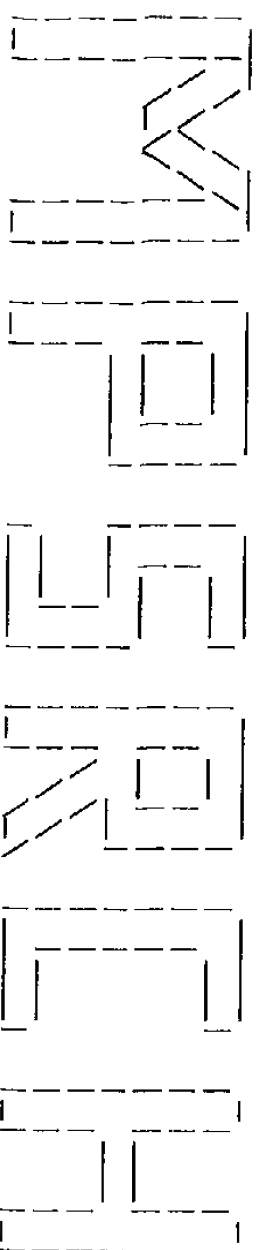
Db 676 -tgttt-cttggcaattctgcatgtgctctagtgttacaacaacagctgcctcaaccagtc 733
    ||  ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 900  GTGGCCGCACTGCACCTGTGCATTTGGCTGGGCTACGCCAACAGCAGCCCTCAACCCGGTT 959

Db 734 ctttatgcatttcttgatgataaaactcca-cgatgcttcagagagttctgt 783
    ||  ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 960  CTCTACGCCCTTCTGTGAGAGAGAACTTCAAGCGCTGTCTCCGCCAGCTCTGT 1010
  
```

Search completed: Tue Aug 26 09:53:09 1997  
 Job time : 286 secs.

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(TM)

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Mpsrch\_p protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Aug 26 07:50:18 1997; MasPar time 14.95 Seconds

Tabular output not generated. 539.070 Million cell updates/sec

Title: >US-08-292-694A-2

Description: (1-380) from US08292694A.pep

Perfect Score: 2839

Sequence: 1 MESPFIQIFRGDPGPTCSPSA.....RNTVQDPASMRDVGGMNKPV 380

Scoring table: PAM 150  
Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot34

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 49.868; Variance 103.252; scale 0.483

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2839	100.0	380	7	OPRK_MOUSE	KAPPA-TYPE OPIOID REC	0.00e+00
2	2829	99.6	380	7	OPRK_RAT	KAPPA-TYPE OPIOID REC	0.00e+00
3	2747	96.8	380	7	OPRK_HUMAN	KAPPA-TYPE OPIOID REC	0.00e+00
4	2610	91.9	380	7	OPRK_MOUSE	KAPPA-TYPE OPIOID REC	0.00e+00
5	1678	59.1	398	7	OPRM_MOUSE	MU-TYPE OPIOID RECEPT	2.74e-303
6	1676	59.0	398	7	OPRM_RAT	MU-TYPE OPIOID RECEPT	7.01e-303
7	1675	59.0	400	7	OPRM_HUMAN	MU-TYPE OPIOID RECEPT	1.12e-302
8	1610	56.7	372	7	OPRD_RAT	DELTA-TYPE OPIOID REC	1.94e-289
9	1608	56.6	372	7	OPRD_HUMAN	DELTA-TYPE OPIOID REC	4.94e-289
10	1597	56.3	372	7	OPRD_MOUSE	DELTA-TYPE OPIOID REC	8.56e-287
11	1473	51.9	367	7	OPRX_RAT	PROBABLE OPIOID RECEPT	1.36e-261
12	1471	51.8	367	7	OPRX_MOUSE	PROBABLE OPIOID RECEPT	3.46e-261
13	1465	51.6	370	7	OPRX_HUMAN	PROBABLE OPIOID RECEPT	5.70e-260
14	1447	51.0	370	7	OPRX_MOUSE	PROBABLE OPIOID RECEPT	2.56e-256
15	980	34.5	391	9	SSR1_MOUSE	SOMATOSTATIN RECEPTOR	2.90e-162
16	978	34.4	391	9	SSR1_RAT	SOMATOSTATIN RECEPTOR	7.27e-162
17	976	34.4	391	9	SSR1_HUMAN	SOMATOSTATIN RECEPTOR	1.82e-161
18	968	34.1	388	9	SSR4_HUMAN	SOMATOSTATIN RECEPTOR	7.18e-160
19	963	33.9	384	9	SSR4_RAT	SOMATOSTATIN RECEPTOR	7.13e-159
20	954	33.6	384	9	SSR4_MOUSE	SOMATOSTATIN RECEPTOR	4.43e-157
21	938	33.0	368	9	SSR2_BOVIN	SOMATOSTATIN RECEPTOR	6.82e-154
22	936	33.0	369	9	SSR2_PIG	SOMATOSTATIN RECEPTOR	1.71e-153

23	927	32.7	369	9	SSR2_RAT	SOMATOSTATIN RECEPTOR	1.05e-151
24	922	32.5	369	9	SSR2_MOUSE	SOMATOSTATIN RECEPTOR	1.04e-150
25	912	32.1	369	9	SSR2_HUMAN	SOMATOSTATIN RECEPTOR	1.01e-148
26	850	29.9	333	4	GPR8_HUMAN	PROBABLE G PROTEIN-CO	2.03e-136
27	819	28.8	363	9	SSR5_HUMAN	SOMATOSTATIN RECEPTOR	2.74e-130
28	815	28.7	418	9	SSR3_HUMAN	SOMATOSTATIN RECEPTOR	1.69e-129
29	792	27.9	328	4	GPR7_HUMAN	PROBABLE G PROTEIN-CO	5.83e-125
30	788	27.8	363	9	SSR3_RAT	SOMATOSTATIN RECEPTOR	3.58e-124
31	734	25.9	428	9	SSR3_MOUSE	SOMATOSTATIN RECEPTOR	1.48e-113
32	732	25.8	428	9	SSR3_MOUSE	SOMATOSTATIN RECEPTOR	3.66e-113
33	639	22.5	359	1	AG2R_CANEA	TYPE-1 ANGIOTENSIN II	5.15e-95
34	629	22.2	359	1	AG2R_HUMAN	TYPE-1A ANGIOTENSIN I	4.49e-93
35	626	22.1	359	1	AG2R_PIG	TYPE-1 ANGIOTENSIN II	1.71e-92
36	623	21.9	355	2	CKR1_HUMAN	C-C CHEMOKINE RECEPTO	6.53e-92
37	617	21.7	359	1	AG2R_RABIT	TYPE-1 ANGIOTENSIN II	9.48e-91
38	616	21.7	359	1	AG2R_BOVIN	TYPE-1 ANGIOTENSIN II	1.48e-90
39	615	21.7	359	1	AG2S_RAT	TYPE-1B ANGIOTENSIN I	2.31e-90
40	614	21.6	349	4	GALR_HUMAN	GALANIN RECEPTOR (GAL	3.61e-90
41	610	21.5	359	1	AG2S_MOUSE	TYPE-1B ANGIOTENSIN I	2.14e-89
42	609	21.5	359	1	AG2R_MOUSE	TYPE-1A ANGIOTENSIN I	3.34e-89
43	609	21.5	359	1	AG2R_MOUSE	TYPE-1 ANGIOTENSIN II	3.34e-89
44	607	21.4	359	1	AG2R_RAT	TYPE-1A ANGIOTENSIN I	8.15e-89
45	586	20.6	362	1	AG2R_XENLA	TYPE-1-LIKE ANGIOTENS	9.21e-85

ALIGNMENTS

RESULT	ID	OPRK_MOUSE	STANDARD;	PRT;	380 AA.
AC	P33534;				
DT	01-FEB-1994 (REL. 28, CREATED)				
DT	01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)				
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)				
DE	KAPPA-TYPE OPIOID RECEPTOR (KOR-1) (MSL-1).				
OS	MUS MUSCULUS (MOUSE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; RODENTIA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-BRAIN;				
RX	MEDLINE; 93342064.				
RA	YASUDA K., RAYNOR K., KONG H., BREDDER C.D., TAKEDA J., REISINE T.,				
RA	BELL G.I.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 95100967.				
RA	NISHI M., TAKESHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;				
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 95251663.				
RA	LIU H.C., LU S., AUGUSTIN L.B., ELSHEIM R.F., CHEN H.C.,				
RA	LOH H.H., WEI L.N.;				
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 209:639-647(1995).				
CC	-!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM				
CC	ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR				
CC	FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF				
CC	AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.				
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
CC	-!- TISSUE SPECIFICITY: BRAIN (NEOCORTEX, HIPPOCAMPUS, AMYGDALA,				
CC	MEDIAL HABENULA, HYPOTHALAMUS, LOCUS CERULEUS, AND PARABRACHIAL				
CC	NUCLEUS).				
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
DR	EMBL; L11065; G348249; -.				
DR	EMBL; D31665; G808876; -.				
DR	EMBL; D31663; G808876; JOINED.				
DR	EMBL; D31664; G808876; JOINED.				
DR	EMBL; S77872; G998532; -.				
DR	EMBL; S77868; G998532; JOINED.				
DR	EMBL; S77869; G998532; JOINED.				
DR	PIR; A48227; A48227.				
DR	GCRDB; GCR_0635; -.				

DR PROSITE; PS00237; G-PROTEIN\_RECEPTOR.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 59 85 1 (POTENTIAL).  
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 96 117 2 (POTENTIAL).  
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 133 154 3 (POTENTIAL).  
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 174 196 4 (POTENTIAL).  
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 223 247 5 (POTENTIAL).  
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 276 299 6 (POTENTIAL).  
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 312 333 7 (POTENTIAL).  
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 131 210 BY SIMILARITY.  
FT LIPID 345 345 PALMITATE (POTENTIAL).  
FT CARBOXYD 25 25 POTENTIAL.  
FT CARBOXYD 39 39 POTENTIAL.  
FT CONFLICT 211 211 S -> L (IN REF. 2 AND 3).  
FT CONFLICT 231 231 F -> V (IN REF. 2 AND 3).  
SQ SEQUENCE 380 AA; 42652 MW; C6F33212 CRC32;  
  
Query Match 100.0%; Score 2839; DB 7; Length 380;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 1 mespiqifrgdpgptcpspacilpnssswfipnwaesdngsvgsedqqlsahispaipy 60  
QY 1 MESPIQIFRGDPGPTCSPSACILPNSSSWFIPNWAESDNGSVGSEDQQLSAHISPAIPV 60  
  
Db 61 itavysvfvvvglyvgnslvmfvilirytkmktatniyifnlaladalvttmpfgsavyi 120  
QY 61 ITAVYSVFEVVGGLVGNSLVMEVILIRYTKMKTATNIYIFNLALADALVTTMPFQSAYVL 120  
  
Db 121 mswpfgdvclckivisidyymftsiftltmmsvdyriavchpykaldfrtplkakiini 180  
QY 121 MNSWPFGDVLCKIVISIDYYMFTSIFTLTMSVDRIYAVCHPYKALDFRTPLEKAKIINI 180  
  
Db 181 ciwllassvgisaivlggtkvrredvdviesclqfpddegyswdlfmkicvtfafvipvl 240  
QY 181 CIWLLASSVGISAIVLGGTKVRREDVDVIECSLQFPDDEYSWMDLFMKICVEYFAVIPVL 240  
  
Db 241 iivvcytlmlrlksvrlsgrskdnrlrrtklavlvaavflicwtpihifilvealg 300  
QY 241 IIVVCYTIMLRKSVRLSGRSREKDRNLRRTKLAVLVAAVFIIICWTPIHIFILVEALG 300  
  
Db 301 stshstaalssyfciaigytnsslnpvllyafldenfkrcfrdfcfcikmmerqstnrv 360  
QY 301 STSHSTAALSSYFCIALGYTNSLNPLVLYAFLDENFKRCFRDFCFIKMRMERQSTNRV 360  
  
Db 361 nrtvqdpasmrdvvgmnpky 380  
QY 361 NRTVQDPASMRDVGGMNPKY 380

RESULT 2  
ID OPRK\_RAT STANDARD; PRT; 380 AA.  
AC P34975;  
DT 01-FEB-1994 (REL. 28, CREATED)  
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).  
GN KOR-D.  
OS RATUS NORVEGICUS (RAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;

RX MEDLINE; 94059008.  
RA CHEN Y., MESTER A., LIU J., YU L.;  
RL BIOCHEM. J. 295:625-628(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 93374033.  
RA MINAMI M., TOYA T., KATAO Y., MAEKAWA K., NAKAMURA S., ONOGI T.,  
RA KANEKO S., SATOH M.;  
RL FEBS LETT. 329:291-295(1993).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;  
RX MEDLINE; 94059009.  
RA LI S., ZHU J., CHEN C., CHEN Y.-W., DERIEL J.K., ASHBY B.,  
RA LIU-CHEN L.-Y.;  
RL BIOCHEM. J. 295:629-633(1993).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;  
RX MEDLINE; 94052210.  
RA MENG F., XIE G.-X., THOMPSON R.C., MANSOUR A., GOLDSTEIN A.,  
RA WATSON S.J., AKIL H.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 90:9954-9958(1993).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WISTAR; TISSUE=BRAIN;  
RX MEDLINE; 93380575.  
RA NISHI M., TAKESHIMA H., FUKUDA K., KATO S., MORI K.;  
RL FEBS LETT. 330:77-80(1993).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY;  
RX MEDLINE; 95204422.  
RA YAKOVLEV A.G., KRUEGER K.E., FADEN A.I.;  
RL J. BIOL. CHEM. 270:6421-6424(1995).  
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR  
FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF  
AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; I22001; G409237; -.  
DR EMBL; D16829; G404116; -.  
DR EMBL; I22536; G425189; -.  
DR EMBL; U00442; G403487; -.  
DR EMBL; D16534; G415310; -.  
DR EMBL; U17995; G727260; -.  
DR EMBL; U17993; G727260; JOINED.  
DR EMBL; U17994; G727260; JOINED.  
DR PIR; S36143; S36143.  
DR PIR; S38825; S38825.  
DR GCRDB; GCR\_0636; -.  
DR GCRDB; GCR\_0724; -.  
DR GCRDB; GCR\_0790; -.  
DR GCRDB; GCR\_0804; -.  
DR PROSITE; PS00237; G-PROTEIN\_RECEPTOR.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 59 85 1 (POTENTIAL).  
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 96 117 2 (POTENTIAL).  
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 133 154 3 (POTENTIAL).  
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 174 196 4 (POTENTIAL).  
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 223 247 5 (POTENTIAL).  
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 276 299 6 (POTENTIAL).  
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 312 333 7 (POTENTIAL).  
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).

FT DISULFID 131 210 BY SIMILARITY.  
FT LIPID 345 345 PALMITATE (POTENTIAL).  
FT CARBOHYD 25 25 POTENTIAL.  
FT CARBOHYD 39 39 POTENTIAL.  
FT CONFLICT 42 42 V -> L (IN REF. 2).  
FT CONFLICT 345 345 C -> Y (IN REF. 3).  
SQ SEQUENCE 380 AA; 42688 MW; EE858A46 CRC32;

Query Match 99.6%; Score 2829; DB 7; Length 380;  
Best Local Similarity 98.9%; Pred. No. 0.00e+00;  
Matches 376; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 mespiqifrgpgptcapsaclpnsswfpnwaesdngsvgsedqglepahispalp 60  
QY 1 MESPIQIFRGDPGPTCSPSACLPNSSWFPNWAESDSNGSVGSEDQQLSAHISPALPV 60  
Db 61 iitavysvfvvlgvgnslvmfvirytckmktatniyifnlaladalvttmpfgsavy 120  
QY 61 IITAVYSVFEVVGVLGNSLVMFVIRYTKMKTATNIYIFNLALADALVTTMPFGSAVYL 120  
Db 121 mmswpgfdvclkiivisidyymftsifltmmsvdryiaavchpykaldfrtplkakini 180  
QY 121 MMSWPGFDVCLKIVISIDYNNFTSIFLTMSVDRIYAVCHPYKALDFRTPLKAKIINI 180  
Db 181 ciwllassvgisaivlgqtkvredvdiesslgfpddeswqifmkicvfvafvipy 240  
QY 181 CIWLLASSVGISAIVLGTKVREDVDIECSLGFPDDEYSWDLFMKICVFVFAFVIPPVL 240  
Db 241 iivcytlimlrlksvrlsgrdknrlritklvllvvavflicwtpihifilvealg 300  
QY 241 IIVCYTLMILRLKSVRLSGRDKNRLRITKLVLVVAVFIIICWTPIHIFILVEALG 300  
Db 301 stshstaalssyyficialgytnslnpvlyafldenfkrcfrdcfpikmmergstnrv 360  
QY 301 STSHSTAALSSYYFICIALGYTNSLNPVLYAFLDENFKRCFRDCEFPKMRMERGSTNRV 360  
Db 361 rntvqdpasmrdvvgmknkv 380  
QY 361 RNTVQDPASMRDVGGMKNKPV 380

RESULT 3  
ID OPRK\_HUMAN STANDARD; PRT; 380 AA.  
AC P41145;  
DT 01-FEB-1995 (REL. 31, CREATED)  
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).  
GN OPRK1 OR OPRK.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RX MEDLINE; 94338360.  
RA MANSSON E., BARE L.A., YANG D.;  
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:1431-1437(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RX MEDLINE; 95350200.  
RA SIMONIN F., GAVERIAUS-RUFF C., BEFORT K., LANNES B., MICHELETTI G.,  
RA MATTEI M.-G., CHARON G., BLOCH B., KIEFFER B.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 92:7006-7010(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE; 95174504.  
RA ZHU J., CHEN C., XUE J.C., KUNAPULI S., DERIEL J.K., LIU-CHEN L.-Y.;  
RL LIFE SCI. 56:201-207(1995).  
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM  
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR

CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF  
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; U11053; G532060; -.  
DR EMBL; U17298; G596070; -.  
DR EMBL; L37362; G722618; -.  
DR PIR; JC2338; JC2338.  
DR MIM; 165196; -.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR.  
DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
KW DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 59 85 1 (POTENTIAL).  
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 96 117 2 (POTENTIAL).  
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 133 154 3 (POTENTIAL).  
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 174 196 4 (POTENTIAL).  
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 223 247 5 (POTENTIAL).  
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 276 299 6 (POTENTIAL).  
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 312 333 7 (POTENTIAL).  
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 131 210 BY SIMILARITY.  
FT LIPID 345 345 PALMITATE (POTENTIAL).  
FT CARBOHYD 25 25 POTENTIAL.  
FT CARBOHYD 39 39 POTENTIAL.  
FT CONFLICT 39 39 POTENTIAL.  
SQ SEQUENCE 380 AA; 42659 MW; 1980629E CRC32;

Query Match 96.8%; Score 2747; DB 7; Length 380;  
Best Local Similarity 93.9%; Pred. No. 0.00e+00;  
Matches 357; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

Db 1 mespiqifrgpgptcapsaclpnssawfipywaepdsngsagedaqlepahispalp 60  
QY 1 MESPIQIFRGDPGPTCSPSACLPNSSWFPNWAESDSNGSVGSEDQQLSAHISPALPV 60  
Db 61 iitavysvfvvlgvgnslvmfvirytckmktatniyifnlaladalvttmpfgsavy 120  
QY 61 IITAVYSVFEVVGVLGNSLVMFVIRYTKMKTATNIYIFNLALADALVTTMPFGSAVYL 120  
Db 121 mmswpgfdvclkiivisidyymftsifltmmsvdryiaavchpykaldfrtplkakini 180  
QY 121 MMSWPGFDVCLKIVISIDYNNFTSIFLTMSVDRIYAVCHPYKALDFRTPLKAKIINI 180  
Db 181 ciwllassvgisaivlgqtkvredvdiesslgfpddeswqifmkicvfvafvipy 240  
QY 181 CIWLLASSVGISAIVLGTKVREDVDIECSLGFPDDEYSWDLFMKICVFVFAFVIPPVL 240  
Db 241 iivcytlimlrlksvrlsgrdknrlritklvllvvavflicwtpihifilvealg 300  
QY 241 IIVCYTLMILRLKSVRLSGRDKNRLRITKLVLVVAVFIIICWTPIHIFILVEALG 300  
Db 301 stshstaalssyyficialgytnslnpvlyafldenfkrcfrdcfpikmmergstnrv 360  
QY 301 STSHSTAALSSYYFICIALGYTNSLNPVLYAFLDENFKRCFRDCEFPKMRMERGSTNRV 360  
Db 361 rntvqdpaylrdidgmknkv 380  
QY 361 RNTVQDPASMRDVGGMKNKPV 380

RESULT 4  
ID OPRK\_CAVPO STANDARD; PRT; 380 AA.  
AC P41144;  
DT 01-FEB-1995 (REL. 31, CREATED)  
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

DE	KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
OS	CAVIA PORCELLUS (GUINEA PIG).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=HARTLEY; TISSUE=BRAIN;
RX	MEDLINE; 94224825.
RA	XIE G.X., MENG F., MANSOUR A., THOMPSON R.C., HOVERSTEN M.T.,
RA	GOLDSTEIN A., WATSON S.J., AKIL H.;
RL	PROC. NATL. ACAD. SCI. U.S.A. 91:3779-3783(1994).
CC	-I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC	ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC	FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
CC	AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR	EMBL; U04092; G476107; .
DR	GCRDB; GCR_0991; .
DR	G-PROTEIN COUPLED RECEPTOR, TRANSMEMBRANE; GLYCOPROTEIN;
KW	PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
KW	DOMAIN
FT	1 58 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 59 85 1 (POTENTIAL).
FT	DOMAIN 96 95 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 96 117 2 (POTENTIAL).
FT	DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 133 154 3 (POTENTIAL).
FT	DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 174 196 4 (POTENTIAL).
FT	DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 223 247 5 (POTENTIAL).
FT	DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 276 299 6 (POTENTIAL).
FT	DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 312 333 7 (POTENTIAL).
FT	DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
FT	LIPID 131 210 BY SIMILARITY.
FT	LIPID 345 345 PALMITATE (POTENTIAL).
FT	CARBOHYD 25 25 POTENTIAL.
FT	CARBOXYD 39 39 POTENTIAL.
SQ	SEQUENCE 380 AA; 42736 MW; F9F34C4C CRC32;
Query Match	91.9%; Score 2610; DB 7; Length 380;
Best Local Similarity	92.9%; Pred. No. 0.00e+00;
Matches 338; Conservative	21; Mismatches 5; Indels 0; Gaps 0;
Dn	17 arnaclpnsgawlpgrwaepdgngsagpqdeglepahispaiavitavysvfvvglyg 76
QY	17 spsacllpnssswfnpmaesdsngsvgsedoqlsahispaipviitavyssvfvgwlv 76
Dn	77 nslvmfviirytkmktatniyifnlaladalvtttmpfgstvylnmswpfgdvlckivis 136
QY	77 nslvmfviirytkmktatniyifnlaladalvtttmpfgsaaylmlnmswpfgdvlckivis 136
Dn	137 idyymftsiftltmmsvdyiaavchpvkaldfrtpikakiniiciwlssvgisaatl 196
QY	137 idyymftsfiftltmmsvdyiaavchpvkaldftrtplkakiniiciwllassvgisaavl 196
Dn	197 cgtkvredvdiecslgfpdddswwdlfmkicvfvafatyipvllliyvcylmilrikvs 256
QY	197 ggtkvredvdviecslgfpepdeswwdlfmkicvfvafatyipvllliyvcylmilrksv 256
Dn	257 rllsgsrekdmrlrrittlrvlvvavfiicwtpihifilvealgstshstaalsyyfcil 316
QY	257 rllsgsrekdmrlrritklrvlvvavfiicwtphifilvealgstshstaalsyyfcil 316
Dn	317 elgytnusslnpilayalfdenfkrcfdcfpikmmersqtsrvntvqdpaymrnvdyv 376
QY	317 algytnusslnpvllyafldenfkrcefrcfpiikrmersqtnrvrntvqpasmrndvvgm 376
Dn	377 rkpy 380

[illegible]





Query	Match	Similarity	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
Db	70	altimalysivcvgvlfgnflvmyvivrytkmktatniyifaladalatsltpfgsvn	66.6%	129	400	207	52	49	3	3
QY	59	pylittavysvvefvgglvngslvmevliirytkmktatniyifenaladalvtttimpfqsav	66.6%	118	400	207	52	49	3	3
Db	130	ylngtwpfgtllckivisidyyumftsiftletmsvdyriavchpvcakaldftprnakil	66.6%	189	400	207	52	49	3	3
QY	119	ylmnsmpfegdvclckivisidyyumftsiftletmsvdyriavchpvcakaldftprnakil	66.6%	178	400	207	52	49	3	3
Db	190	nycnwilssaisglpvmfmattkyrgg-s-idctltfsbptw-ywenlvkicvfiifafimp	66.6%	246	400	207	52	49	3	3
QY	179	nicimwlassvgisaisglpvmfmattkyrgg-s-idctltfsbptw-ywenlvkicvfiifafimp	66.6%	238	400	207	52	49	3	3
Db	247	vliitvcyglmllrlksvrmlsgskekdnlrritrmvllvvavfivcwtpihivliika	66.6%	306	400	207	52	49	3	3
QY	239	vliitvcyglmllrlksvrmlsgskekdnlrritrmvllvvavfivcwtpihivliika	66.6%	298	400	207	52	49	3	3
Db	307	lvitpelttftqsvwhfcialgytuncslnpvlyafldenfkrcrfrefcicptsniqgnst	66.6%	365	400	207	52	49	3	3
QY	299	lgsitshstaaalssyyfcialgytuncslnpvlyafldenfkrcrfrefcicptsniqgnst	66.6%	358	400	207	52	49	3	3

```

Db      367 rirgntdrhps 377
      |:|:|:|:|
QY      359 rvrntvQDPAS 369

RESULT      8
ID   OPD_RAT      STANDARD;      PRI;      372 AA.
AC   P33533;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   DELTA-TYPE OPIOID RECEPTOR (DOR-1) (OPIOID RECEPTOR A).
FOR-A.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 93351652.
RA   FEUKDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;
RL   FEBS LETT. 327:311-314(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX   MEDLINE; 94322412.
RA   ABOOD M.E., NOEL M.A., FARNSWORTH J.S., TAO Q.;
RL   J. NEUROSCI. RES. 37:714-719(1994).
CC   -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC   ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
CC   STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.
CC   -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; D16348; G391865; -.
DR   EMBL; U00475; G514211; -.
DR   PIR; S34592; S34592.
DR   GCRDB; GCR_0638; -.
DR   GCRDB; GCR_0805; -.
DR   PROSITE; PS00237; G-PROTEIN_RECEPTOR.
KW   G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW   PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT   DOMAIN      1      45      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   46      75      1 (POTENTIAL).
FT   DOMAIN      76      84      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   85      102     2 (POTENTIAL).
FT   DOMAIN      103     124     EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   125     144     3 (POTENTIAL).
FT   DOMAIN      145     174     CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   175     190     4 (POTENTIAL).
FT   DOMAIN      191     215     EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   216     238     5 (POTENTIAL).
FT   DOMAIN      239     261     CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   262     284     6 (POTENTIAL).
FT   DOMAIN      285     293     EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   294     310     7 (POTENTIAL).
FT   DOMAIN      311     372     CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    18      18      POTENTIAL.
FT   CARBOHYD    33      33      POTENTIAL.
FT   CARBOHYD    121     198     BY SIMILARITY.
FT   DISULFID    333     333     PALMITATE (POTENTIAL).
FT   LIPID        372 AA; 40449 MW; 59F5EE50 CRC32;

Query Match      56.7%; Score 1610; DB 7; Length 372;
Best Local Similarity 65.6%; Pred. No. 1,94e-289;
Matches 214; Conservative 55; Mismatches 48; Indels 9; Gaps 7;

Db      15 llavnsdtfpaafpsasanasgspgar--sas-slalalalalysavcavglignvlym 71
      ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY      22 LLPNSSWFPNMAESDSNGSVGSEDDQLLESAHISPAIPVITTAVYGVYVGLVGNLVM 81
      |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
      fgivvytkiktatniyifnlaladalatstlpfgsakylmetwpgfelickavlsidynn 131
      |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

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DQ		82	FVIRYTKMKATNTNITYIFNLALADALTVTMTTFQSAAVLIMNSWPFGDYLCKIVISIDYYN	141
Dd		132	mfsisftlmtmsvdryiavcchpvkaldfrtpakaliniiciwlasgygvpimavtqp	191
OY		142	METSIFTLTMSVDRIYAACHPVKALDEFRPLAKIINICIWLASSVGISAIVLGSTKV	201
Dd		192	rôga-vv-ctlgfpp--swywdvtvkicvfalfafvwpililitvcygmlrlsvrlls	247
OY		202	KEDVDVIECSLQFPDDEYSW-WDLFMKCIVEFAFVIPVLIIVCYTLMILRKSVRLS	260
Dd		248	gskekdrslrritlmvlvvvgafvccapinhivwtlvdiinrdplvyaalhlcialg	307
OY		261	GSRBKDRMLRRITKLVLVVAVAFIIICWTPIHIFILEVALGSTSHSTA-ALESSYFCIALG	319
Dd		308	yansslnpvlyafldenfkrcfrqlc	333
OY		320	YNSSLNPVLYAFLDENFKRCFRDFC	345
RESULT	9			
ID	OPRD_HUMAN	STANDARD;	PRT; 372 AA.	
AC	p41143;			
DT	01-FEB-1995 (REL. 31, CREATED)			
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)			
DT	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)			
DN	DELTA-TYPE OPIOID RECEPTOR (DOR-1).			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=CEREBRAL CORTEX, AND STRIATUM;			
RX	MEDLINE; 94260835.			
RA	KNAPP R.J., MALATYNSKA E., FANG L., LI X., BABIN E., NGUYEN M., SANTORO G., VARGA E.V., HRUBY V.J., ROESKE W.R., YAMAMURA H.I.; LIFE SCI. 54:463-469(1994).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 95107267.			
RA	SIMONIN F., BEFORT K., GAVERLAUX-RUFF C., MATTHES H., NAPPEY V., LANNES B., MICHELETTI G., KEEFER B.;			
RL	MOL. PHARMACOL. 46:1015-1021(1994).			
CC	-1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR	EMBL; U07882; G497314; - .			
DR	EMBL; U10504; E162517; - .			
DR	MIT; 165195; - .			
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR.			
KW	G-PROTEIN COUPLE D RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION; LIPOPOTEIN; PALMITEATE.			
KW	DOMAIN 1	45	EXTRACELLUL AR (POTENTIAL) .	
FT	TRANSSEM	46	75	1 (POTENTIAL) .
FT	DOMAIN	76	84	CYTO PLASM IC (POTENTIAL) .
FT	TRANSSEM	85	102	2 (POTENTIAL) .
FT	DOMAIN	103	124	EX TR AC EL LU LA R (POTENTIAL) .
FT	TRANSSEM	125	144	3 (POTENTIAL) .
FT	DOMAIN	145	174	CYTO PL ASM IC (POTENTIAL) .
FT	TRANSSEM	175	190	4 (POTENTIAL) .
FT	DOMAIN	191	215	EX TR AC EL LU LA R (POTENTIAL) .
FT	TRANSSEM	216	238	5 (POTENTIAL) .
FT	DOMAIN	239	261	CYTO PL ASM IC (POTENTIAL) .
FT	TRANSSEM	262	284	6 (POTENTIAL) .
FT	DOMAIN	285	293	EX TR AC EL LU LA R (POTENTIAL) .
FT	TRANSSEM	294	310	7 (POTENTIAL) .
FT	DOMAIN	311	372	CYTO PL ASM IC (POTENTIAL) .
FT	CARB OH YD	18	18	POTENTIAL .
FT	CARB OH YD	33	33	POTENTIAL .
FT	DISU LF ID	121	198	BY SI MI LA RI TY .
FT	LIPID	333	333	P ALMI TE AT E (POTENTIAL) .

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FT CONFLICT 27 27 F -> C (IN REF. 2).
FT CONFLICT 40 41 PG -> AR (IN REF. 2).
FT CONFLICT 348 348 P -> A (IN REF. 2).
FT CONFLICT 370 370 R -> A (IN REF. 2).
SQ SEQUENCE 372 AA; 40450 MW; CFF92985 CRC32;

Query Match          56.6%; Score 1608; DB 7; Length 372;
Best Local Similarity 65.3%; Pred. No. 4,94e-289;
Matches 213; Conservative 56; Mismatches 48; Indels 9; Gaps 8;

Db      15 lfnasdays-a-fpsaganasgppgpsas-slalaiaitalysavcavgllgnlym 71
QY      22 LRPNSSWFEPNMAESDSNGSVGSEDQLESASHISPAIPVITTAIVYSVFVGVLGNLSLYM 81
Db      72 fgivrytkmkatniyiflnaladatatstlpfqsakylmetwpgellckavlsidynn 131
QY      82 FVIRTYTKMTATNIYIFNLALADALVTITMPFQSAYVLMNSWPFQDVLCIKIVISIDYYN 141
Db      132 mfsisiftlmnsvdryiavchpvkalditfpakaliniciwlasgygyymavrrp 191
QY      142 MFTSIFTLTMSVDRIYAVCHPVKALDEPRTPLKAKIINICIMWLASSVGISAIVLGSTKY 201
Db      192 rdga-vv-cmlqgfsp--swywdtvcikcvlfafvvpililtvcyglmllrlsvrlls 247
QY      202 REDVDVIECSLQFPDDEYSW-WDLFMKICVEFAFVILPVLIITVCYTMLRLKSYLLS 260
Db      248 gskedrsllritrmvlvvvgafvwcwapihifvivwtlvldidrrdpjvwaaahlcialg 307
QY      261 GSREDRNLRLRITKLVLVVVAVFIICTWPIHIFILVEALGSTSHSTA-ALSSIFYCIALG 319
Db      308 yansslnpvlyafidenfkrcfrqlc 333
QY      320 YTNSSLNPVLYAFLDENFKRCFRDFC 345

RESULT 10
ID OPND.MOUSE STANDARD; PRT; 372 AA.
AC P32300;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1) (K56) (MSL-2).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93101664.
RA KIEFFER B.L., BEFORT K., GAVERIAUX-RUFE C., HIRTH C.G.;
RL PROC. NATL. ACAD. SCI. U.S.A. 89:12048-12052(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93110361.
RA EVANS C.J., KEITH D.E. JR., MORRISON H., MAGENDZO K., EDWARDS R.H.;
RL SCIENCE 258:1952-1955(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE-BRAIN;
RC MEDLINE; 93342064.
RA YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,
RA BELI G.I.;
RL PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).
RN [4]
RP SEQUENCE FROM N.A.
RA KEITH D.E. JR., ANTON B., EVANS C.J.;
RL PROC. WEST. PHARMACOL. SOC. 36:299-306(1993).
RN [5]
RP SEQUENCE OF 8-372 FROM N.A.
RX MEDLINE; 94022364.
RA BADEGA T., CHIN H., KIM K., JUNG H.H., KOZAK C.A., KLEE W.A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 90:9305-9309(1993).
RN [6]
RP 3D-STRUCTURE MODELLING.
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DR GCRDB; GCR\_0912; -  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 48 74 1 (POTENTIAL).  
FT DOMAIN 75 84 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 85 106 2 (POTENTIAL).  
FT DOMAIN 107 121 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 122 143 3 (POTENTIAL).  
FT DOMAIN 144 162 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 163 185 4 (POTENTIAL).  
FT DOMAIN 186 208 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 209 233 5 (POTENTIAL).  
FT DOMAIN 234 261 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 262 285 6 (POTENTIAL).  
FT DOMAIN 286 297 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 298 319 7 (POTENTIAL).  
FT DOMAIN 320 366 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 120 197 BY SIMILARITY.  
FT LIPID 331 331 PALMITATE (POTENTIAL).  
FT CARBOHYD 21 21 POTENTIAL.  
FT CARBOHYD 26 26 POTENTIAL.  
FT CARBOHYD 36 36 POTENTIAL.  
FT CONFLICT 105 105 G -> R (IN REF. 2).  
FT CONFLICT 226 226 L -> V (IN REF. 2).  
FT CONFLICT 246 246 S -> P (IN REF. 2).  
FT CONFLICT 348 348 S -> T (IN REF. 3).  
SQ SEQUENCE 367 AA; 40523 MW; 7FD40CCC CRC32;

Query Match 51.9%; Score 1473; DB 7; Length 367;  
Best Local Similarity 59.3%; Pred. No. 1.36e-261;  
Matches 188; Conservative 63; Mismatches 61; Indels 5; Gaps 5;

Db 40 safipiglkvtiavglyavcigllgnclymyvllrhtkmtatnlyifnlaladtlvl 99  
QY 51 SAHISPAIPVITAVSVFVGVGLVNSLVFVITRYTKMTATNITVFNLAADALVTT 110  
Db 100 tlpfgtdlllgfwpgnalcktviaidymnfstftltamsvdryvaichpiraldvr 159  
QY 111 TMPFQSAVYLMNSWPFGLCKIVISIDYNNMETSIFTLTMSVDRYLAVCHPVKALDFR 170  
Db 160 tsskagavnaivalasvvgvpvaimgsqv-ede-icelveipagdy-wgprfa-ic 215  
QY 171 TPLKAKIINICWILLASSVGSISAIVLGGIVREDVDVIECSLQFPD-DEYSWWDLFMKIC 229  
Db 216 iflfsfipvllisvcyslmirrlrgvrlisgskrdnrlrtrtlrvlrvavfvgcwtp 275  
QY 230 VFVFAVPIVLIITVCTLMILRLKSVRLISGSREKDRNLRLITKLYLVVAVFIICWTP 289  
Db 276 vqvfvlgvlgvpgsetavairlftalgyvnsclnpliyafldenfkacfrkfccass 335  
QY 290 IHIFILVEALGSTSHSTAALSSYFICIALGYTNSLNPLYAFLDENFKRCFRDFCFPIK 349  
Db 336 lhremqvsvdrvsiakd 352  
QY 350 MRMERQSTNRYRNTVQD 366

RESULT 12  
ID OPRX\_MOUSE STANDARD; PRT; 367 AA.  
AC P35377;  
DT 01-JUN-1994 (REL. 29, CREATED)  
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE PROBABLE OPIOID RECEPTOR (ORGC).  
GN OOR.  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6N; TISSUE=BRAIN;

RA YASUDA K., JONES E., REISINE T., BELL G.I.;  
RL SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95100967.  
RA NISHI M., TAKESHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;  
RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;  
RA MATTHEWS H.W.D.;  
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
RN [4]  
RP SEQUENCE OF 1-357 FROM N.A.  
RC STRAIN=BALB/C; TISSUE=SPLEEN;  
RA HALFORD W.P., GEBHARDT B.M., CARR D.J.J.;  
RL SUBMITTED (AUG-1994) TO EMBL/GENBANK/DBJ DATA BANKS.  
CC -1- FUNCTION: OPIOID RECEPTOR WITH A POTENTIAL ROLE IN MODULATING A  
CC NUMBER OF BRAIN FUNCTIONS, INCLUDING INSTINCTIVE BEHAVIOURS AND  
CC EMOTIONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS  
CC WHICH INHIBITS ADENYL CYCLASE.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; U04952; G440880; -.  
DR EMBL; D31667; G808874; -.  
DR EMBL; D31666; G808874; JOINED.  
DR EMBL; X91813; G1008982; -.  
DR EMBL; U14165; G540093; -.  
DR GCRDB; GCR\_0891; -.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR.  
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;  
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.  
FT DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 47 47 EXTRACELLULAR (POTENTIAL).  
FT ORGANISM 1 47 ual\_isolate p5aa) umbilical vein cdna to mRNA.  
REFERENCE 1 (bases 1 to 3081)  
AUTHORS Yousoufian,H., McAfee,M. and Kwiatkowski,D.J.  
TITLE Cloning and chromosomal localization of the human cytoskeletal  
alpha-actinin gene reveals linkage to the beta-spectrin gene  
JOURNAL Am. J. Hum. Genet. 47 (1), 62-71 (1990)  
MEDLINE 90274024  
FEATURES  
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112.2790  
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/product="alpha-actinin"  
/db\_xref="pid:g178052"  
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DLAEKFRQKASIHAWTDGKEAMLROKDYETATISEIKALKLKHEAFESDLAAHQDR  
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VDPNRLGVVITQAEFIDFMSRETADITDADQYMASFKILAGDKNYITMDLRLRLPQD  
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3081

polya\_site



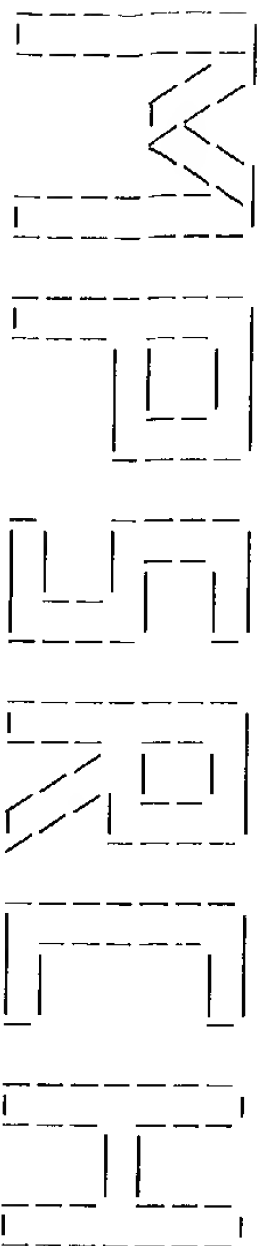
APPLICANT: FAILLA, Cristina  
APPLICANT: TOMEI, Licia  
TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE  
TITLE OF INVENTION: PROTEOLYTIC ACTIVITY OF THE NS3 HEPATITIS C VIRUS (HCV)  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,356  
FILING DATE: 23-AUG-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: DE FRANCESCO=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 631 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-700-356-1  
APITAYSQOTRGILGCLITSLTRDKNOVEGEVYSTATQSFSLATCVNGVCMTYYHGAGSKTLAAPKCP  
ITQMTYNVDQDLVGMFKPPGARSLTPTCTGSSDLVTRHADVIPRRRGDSRLSPRPVSYLKGSSG  
GPLCPFGHVGIFRAAVCTRGVAKAVDFVPESEMTMRSPVFTDNSSPPAVQSFQVAHLHAPTGSGK  
STKVPAAYAAQGIKYLINPSVAATLGFAGYMSKAHQIDENIRTVRTITTGAPVTVSTYGFADGGCS  
GGAYDIIICDECHSTIDSTTILIGTVLDQAEIAGARLVVLATATPPGSVTVPHNIEVALSNTGEIPFY  
GKAIPIEAIRGGRLIFCHSKKKCKDELAAKLSGLINAVAYYRGLDVSVIPIIGDVVVAATDALMTGYTG  
DEDSVIDCNTCVITVDPSLDPFTTETITTVPDVAVSQRGRGTGRGRIYRFVTPGERPSGMFDSY  
LCECYDAGCAWYELTPTAFTSVRLRAYLNTPLPYQODHLEFWESVFTGLTHDAHFLSQTKQAGDNFPYL  
VAYQATVCARAQAPPPSWDQWKCLIRKPTLHGPTPLLYRLGAVQNEVTLTHPTIKYIMACMSADLEVV  
T1

Sequence 2, Application US/08700356  
GENERAL INFORMATION:  
APPLICANT: DE FRANCESCO, Raffaele  
APPLICANT: FAILLA, Cristina  
APPLICANT: TOMEI, Licia  
TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE  
TITLE OF INVENTION: PROTEOLYTIC ACTIVITY OF THE NS3 HEPATITIS C VIRUS (HCV)  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,356  
FILING DATE: 23-AUG-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: DE FRANCESCO=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 54 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-700-356-2  
STWLVGVLAALAAYCLTTGSVIVGRIISGRPAIVPDRELLYQEFDEMEEC1

; Sequence 3, Application US/08700356  
; GENERAL INFORMATION:  
; APPLICANT: DE FRANCESCO, Raffaele  
; APPLICANT: FALLA, Cristina  
; APPLICANT: TOMEI, Licia  
; TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE  
; TITLE OF INVENTION: PROTEOLYTIC ACTIVITY OF THE NS3 HEPATITIS C VIRUS (HCV)  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,356  
; FILING DATE: 23-AUG-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: DE FRANCESCO=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: /note="Xaa at position 34 means  
; OTHER INFORMATION: Abu (2-Aminobutyric acid)"  
; US-08-700-356-3  
; GSVIVIGRIILSGRPAIVPDREVLVQEFDEMEEX1

CC were used in the isolation of the NS2-NS4 regions of the Hepatitis C  
CC Virus (HCV) gene of the invention (see also R29660, R29559-60 and  
CC R29843-51). These RNA sequences were isolated from the serum of a  
CC patient suffering from hepatitis C (HC). The isolated RNA sequences  
CC were converted into cDNA using transcriptase in the presence of one  
CC of the primer sequences given in Q32578-79. The sequences were then  
CC amplified using primer pairs. The cDNA sequences isolated represent  
CC different alleles of the same region of the HCV





\*\*\*\*\*

Release 2.1D John F. Collins, Bloocomputing Research Unit.  
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Mpsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Aug 26 14:43:42 1997; Maspar time 9.43 Seconds

Tabular output not generated. 460.872 Million cell updates/sec

Title: >US-08-292-694A-2  
Description: (1-380) from US08292694A.pep  
Perfect Score: 2839  
Sequence: 1 MESPFIQIFRGDPGPTGCSFA.....RNTYQDPASMRDVGGMKRPV 380

Scoring table: PAM 150  
Gap 11

Searched: 96640 seqs, 11439865 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq27  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20

Statistics: Mean 34.629; Variance 152.210; scale 0.228

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2839	100.0	380	13	R67669	Mouse kappa opioid re
2	2829	99.6	380	14	R76783	Rat kappa opiate rece
3	2823	99.4	380	14	R72591	Mammalian kappa opioi
4	2746	96.7	380	17	R88722	Human kappa opioid re
5	2130	75.0	295	12	R67672	Human kappa opioid re
6	1583	59.3	356	11	R65188	Human mu-subtype opi
7	1677	59.1	400	13	R71966	Human mu opioid recep
8	1676	59.0	398	14	R76781	Rat mu opiate recepto
9	1674	59.0	398	13	R71964	Rat mu opioid recepto
10	1675	59.0	400	14	R76780	Human mu opiate recep
11	1610	56.7	372	14	R76782	Rat delta opiate rece
12	1597	56.3	372	13	R67670	Mouse delta opiate re
13	1597	56.3	372	9	R48629	Sequence of murine de
14	1499	52.8	371	10	R66503	Murine delta opioid r
15	1473	51.9	367	13	R71968	Rat opioid receptor.
16	1471	51.8	367	13	R67671	Mouse opioid receptor
17	1464	51.6	367	14	R76638	Rat opiorph receptor
18	1195	42.1	367	13	R74298	Mouse kappa-3 opioid
19	980	34.5	391	7	R39260	Murine somatostatin r
20	976	34.4	391	7	R39259	Human somatostatin re

21	922	32.5	369	7	R39262	Murine somatostatin r	1.88e-74
22	912	32.1	369	19	R97269	Human somatostatin re	1.70e-73
23	912	32.1	369	7	R39261	Human somatostatin re	1.70e-73
24	901	31.7	369	5	R27504	Pituitary somatostati	1.91e-72
25	850	29.9	333	13	R72985	Epsilon opioid recept	1.40e-67
26	817	28.8	322	19	W02726	Rat RGHF G-protein c	1.95e-64
27	817	28.8	322	16	R48754	Rat RGH G-protein cou	1.95e-64
28	815	28.7	418	7	R39263	Human somatostatin re	4.65e-62
29	792	27.9	328	13	R72984	Epsilon opioid recept	4.65e-62
30	732	25.8	428	7	R39264	Murine somatostatin r	2.30e-56
31	623	21.9	355	11	R52749	C-C chemokine recepto	4.50e-46
32	614	21.6	349	18	R95070	Human galanin recepto	3.16e-45
33	614	21.6	349	14	R79443	Galanin receptor.	3.16e-45
34	603	21.2	325	16	R48730	G-protein coupled bov	3.41e-44
35	603	21.2	325	19	W02702	G-protein coupled bov	3.41e-44
36	588	20.7	348	18	R95069	Mouse pancreas beta-c	8.70e-43
37	588	20.7	348	17	R91229	Mouse pancreas G-prot	8.70e-43
38	587	20.7	355	18	W03376	CC-chemokine receptor	1.08e-42
39	584	20.6	355	18	W03377	CC-chemokine receptor	2.06e-42
40	575	20.3	359	9	R44531	Human angiotensin II	1.44e-41
41	573	20.2	402	18	R98358	Somatostatin-like rec	2.21e-41
42	569	20.0	355	18	W03378	Human angiotensin II	1.44e-41
43	562	19.8	352	20	W07602	CC-chemokine receptor	5.24e-41
44	554	19.5	380	10	R53750	Human G-protein chemo	2.37e-40
45	550	19.4	363	13	R66934	Seven transmembrane r	1.33e-39
						Mouse AT2 receptor.	3.14e-39

ALIGNMENTS

RESULT 1  
ID R67669 standard; Protein; 380 AA.  
AC R67669;  
DT 17-AUG-1995 (first entry)  
DE Mouse kappa opioid receptor MOR1.  
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;  
KW transmembrane domain; somatostatin; receptor; human; expression vector;  
KW truncate; chimeraic; assay; probe.  
OS Mus musculus.  
PN W09428132-A.  
PD 08-DEC-1994.  
PE 20-MAY-1994; U05747.  
PR 20-MAY-1993; US-066296.  
PR 30-JUL-1993; US-100694.  
PR 05-NOV-1993; US-147592.  
PA (ARCH-) ARCH DEV CORP.  
PI Bell GI, Reisine T, Yasuda K;  
DR WPI; 95-022804/03.  
DR N-PSDB; Q75926.  
PT Polynucleotides and peptides derived from opioid receptor  
PT polypeptides - for use in therapeutic compositions and in  
PT screening assays for useful drug substances.  
PS Claim 8; Page 207-211; 300pp; English.  
CC The amino acid sequence of the novel mouse kappa opioid receptor MOR1.  
CC The corresponding gene was isolated from a mouse brain cDNA library using  
CC a fragment (amplified from the cDNA library with primers Q75929-30) as a  
CC probe. The primers are based on the conserved sequences present in the  
CC second and third transmembrane domains of somatostatin (SRIF) receptor  
CC subtypes SST1, SST2 and SST3. The 1.2 kb pStI fragment from the mouse  
CC kappa opioid receptor clone, lambda ms1-1, was subcloned into the CMV  
CC promoter-based expression vector pCMV-6b. The resultant construct  
CC pCMV-ms1-1 was transfected into COS-1 cells for protein production. The  
CC gene encoding the opioid receptor can be used to produce complete,  
CC truncated or chimeraic opioid receptor proteins. The opioid receptors  
CC thus produced are useful for the development of novel assays designed to  
CC select or improve substances, capable of interacting with the opioid  
CC receptor proteins, for use in diagnosis, drug design and therapeutic  
CC applications.  
SQ Sequence 380 AA;

Query Match 100.0%; Score 2839; DB 13; Length 380;  
Best Local Similarity 100.0%; Pred. No. 1.63e-260;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	mespiqifrgdpptcpspsacilpnssswfpwnaesdngsvgsedqqlsahispaipv	60
Qy	1	MESPIQIFRGDPPTCSPSACILPNSSSWFPWNAESDNGSVGSEDOQLSAHISPAIPV	60
Db	61	litavsvfvvgvlvgnslvmfviirytkmktatniyfnaladalvtttmpfgsavyl	120
Qy	61	LITAVSVFVVGVLVGNSLVMFVIIRYTKMKTAINIYFNALADALVTTTMPFGSAVYL	120
Db	121	mnswpfgdvlokvivisidyymnftsiftlmmsvdryiavchpvykaldftrtpkakiini	180
Qy	121	MNSWPFGBVLCKIVISIDYYNMFTSIFLTMMSSVDRIYAVCHPVKALDFTRTPKAKIINI	180
Db	181	ciwlassvgisaivlgtkvredvdviecslgfpdedswwdlfmkicvfafavipvl	240
Qy	181	CIWLLASVGISAVLGGTKVRBDVDVIECSLGFPDDEYSWWDLFMKICVFAFAVIPVL	240
Db	241	liivcytlmilrlksvrllsgsrekdnrlritklivlvavavfiicwtphihifilvealg	300
Qy	241	LIIVCYTLMILRLKSVRLLSGSREKDRNLRRITKLVLVAVAVFIICWTPHIHIFIVEALG	300
Db	301	stshstaalssyfcialgytnslnpvlyafldenfkrcfrdfocfikmmerqstnrv	360
Qy	301	STSHSTAALSSYFCIALGYTNSLNPVLYAFLDENFKRCRDFOCPIKMRMERQSTNRV	360
Db	361	rintvgdpsamrdvvggmukpv	380
Qy	361	INTVQDPASMRDVGGMUKPV	380

RESULT 2  
 ID R76783; standard; Protein; 380 AA.  
 AC R76783;  
 DT 11-DEC-1995 (first entry)  
 DE Rat kappa opiate receptor.  
 KW Kappa opiate receptor; mu opiate receptor; hMOR; opiate agonist;  
 KW opiate antagonist; drug abuse; analgesic.  
 OS Rattus sp.  
 PN W09520667-A1.  
 PD 03-AUG-1995.  
 PF 30-JAN-1995; U01144.  
 PR 28-JAN-1994; US-188275.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (USSH ) US SEC DEPT HEALTH.  
 PI Johnson PS, Persico AM, Uhl G, Wang J;  
 DR WPI: 95-275452/36.  
 PT New DNA encoding human mu opiate receptor - used esp. for screening  
 PT cpds. for activity as opiate agonists or antagonists  
 PS Disclosure; Page 29-30; 49pp; English.  
 CC hMOR cDNA was obtd. from a human cerebral cortical cDNA library  
 CC screened with fragments of a rat mu opiate receptor. The encoded  
 CC protein showed homology to rat mu, delta and kappa opiate  
 CC receptors (R76781-83).  
 SQ Sequence 380 AA;

Query Match	99.6%;	Score 2829;	DB 14;	Length 380;
Best Local Similarity	98.9%;	Pred. No. 1.55e-259;		
Matches	376;	Conservative	3;	Mismatches 1; Indels 0; Gaps 0;
Db	1	mespiqifirgepgptcapsacallpnssswfpnwaesdsngsvgsedqglepahispaipv	60	
QY	1	MESPIQIFRGDPGPTCSPSACLLPNSSSWFPNWAESDSNGSVGSHDQGLESAHISPAIPV	60	
Db	61	ltavysvfvfvgjlvgnslvmfviirytkmktatniyifnialadalvtttmpfqsavy1	120	
QY	61	LTAVYSVVFVVGJLVGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTMPFQSAVYL	120	
Db	121	mnswpfgdvlckivisidgynmftsifltmmsvdryiaavchpvaikaldfrtp1kakini	180	
QY	121	MNSWPFQDVLCKIVISIDYNNMFTSIFLTMMMSVDRIAVCHPVALDFRTP1KAKIINI	180	
Db	181	ciwllassvgisaivlggtkvredvdviesclqfpddeyswvdlfmkicvfvafov1pvl	240	
QY	181	C1WLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWVDFLMDKICVFVFAFV1PVL	240	

Db	241	liivcytlmlrlkxvrlsgsrekdrnlrrlcklvlvvavfllcwtphihifilvealg	300
QY	241	liivcytlmlrlkxvrlsgsrekdrnlrrlcklvlvvavfllcwtphihifilvealg	300
Db	301	stshstavlssyyfcialgntnsslnpvlafldenfrcfdfcfpikmmergsturv	360
QY	301	stshstavlssyyfcialgntnsslnpvlafldenfrcfdfcfpikmmergsturv	360
Db	361	ntlvqdpasmrdivgmnkpv	380
QY	361	ntlvqdpasmrdivgmnkpv	380

RESULT	3	
ID	R72591	standard; Protein; 380 AA.
AC	R72591;	
DT	01-DEC-1995	(first entry)
DE	Mammalian kappa opioid receptor protein.	
KW	Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic; amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.	
OS	Rattus rattus.	
FH	Key	Location/Qualifiers
FT	CDS	111..1253
FT	/*tag= a	
FT	/product= kappa opioid receptor	
PN	J07070191-A.	
PD	14-MAR-1995.	
PE	30-JUL-1993; 190261.	
PR	09-JUL-1993; JP-170591.	
PA	(TAKE ) TAKEDA CHEM IND LTD.	
DR	WPI; 95-144857/19.	
DR	N-PSDB; Q86725.	
PT	Kappa opioid receptor protein and cells expressing it - useful	
PT	for the screening of compounds for analgesic and hypnotic	
PT	properties	
PS	Claim 2; Page 9-10; 15pp; Japanese.	
CC	The amino acid sequence of the novel mammalian kappa opioid receptor.	
CC	The gene was isolated by amplifying a fragment from rat brain mRNA by	
CC	reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from	
CC	the mouse delta-opioid receptor gene. This fragment was cloned into the	
CC	plasmid pCRII to produce pRII. The plasmid pRII was used to probe a rat	
CC	brain DNA library in lambda ZAPII to obtain a clone of the rat kappa	
CC	opioid receptor gene, designated pKOPR2. This clone was introduced into	
CC	E.coli JM109 for production of the receptor protein. The receptor protein	
CC	is useful for screening of analgesic and hypnotic compounds including	
CC	peptides and proteins.	
CC	Sequence 380 AA;	
CC	SQ	

```

Query Match          99.4%; Score 2823; DB 14; Length 380;
Best Local Similarity 98.7%; Pred. No. 5,98e-259;
Matches 375; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 1 mespiqifrgpgptcapsacclpnssswfpmwaedsngslgsedqglepahispaipv 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 MESPIQIFRGDPGPTCSPSACLDPNSSSWFPMWAESDSNGSVSEDDQLSAHISPAIPV 60

Db 61 itavysvfvvglvgnslvmfvilrlytkmktatniyifnlaladalvtltmpfgsavy 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 IITAVYSVFEVVGVLVGNSLVMEFVILIRYTKMKTATNIYIFNLALADALVTTTMPFGSAVYL 120

Db 121 mswpfgdvclckivisidyamftsiftltnmsvdryiavchpvaikaldfrtplkakini 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 MNSWPFGLCKIVISIDYNNMFTSIFTLTNMSVDRIAVCHPVAIKALDERTPLKAKIINI 180

Db 181 ciwllassvgisaivlggtkvredvdyieoslqfpddeyswcdlfnkicvfvfafavipvl 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 CIWLLASSVGISAIVLGGTKVREDVDYIECSLQFPDDEYSWCDLFMKICVFVFAFVIVPVL 240

Db 241 itivcytlmlrlksvrlllsgsrekdnrlrritklvllvvavflicwtpihifilvealg 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 IITVCYTLMLRLKSVRLLLSGSREKDNRLRRITKLVLLVVAVFIIICWTPIHIFILVEALG 300

```



ID R65188 standard; protein; 356 AA.  
AC R65188;  
DT 19-APR-1995 (first entry)  
DE Murine mu-subtype opioid receptor.  
KW Mu-subtype opioid receptor; MSOR; drug addiction.  
OS Rattus rattus.  
FH Key Location/Qualifiers  
FT Modified\_site 10..12  
FT /note= "putative N-linked glycosylation site"  
FT Modified\_site 230  
FT /note= "Threonine residue especially favourable  
FT for protein kinase A phosphorylation"  
FT Region 25..48  
FT /note= "hydrophobic membrane spanning region"  
FT Region 58..78  
FT /note= "hydrophobic membrane spanning region"  
FT Region 96..118  
FT /note= "hydrophobic membrane spanning region"  
FT Region 139..166  
FT /note= "hydrophobic membrane spanning region"  
FT Region 187..212  
FT /note= "hydrophobic membrane spanning region"  
FT Region 236..257  
FT /note= "hydrophobic membrane spanning region"  
FT Region 274..294  
FT /note= "hydrophobic membrane spanning region"  
PN EP-612845-A.  
PD 31-AUG-1994.  
PF 09-FEB-1994; 101968.  
PR 26-FEB-1993; US-026140.  
PA (AMCY ) AMERICAN CYANAMID CO.  
PI Corbett MJ, Eppler CM, Shieh H, Zysk JR;  
DR N-PSDB; Q79199.  
PT Pure mu-type opioid receptor protein - and nucleic acid coding  
PT for it  
PS Claim 2: Fig 9: 39pp; English.  
CC R65188 is the rat mu-subtype opioid receptor protein purified  
CC from rat brain membranes, with biotinyl-b-endorphin (R56666)  
CC as its ligand. It is encoded by the nucleotide sequence Q79199  
CC which was synthesised using Q71022 and Q71023 as PCR primers.  
CC R65188 is useful for identifying the receptor subtypes, for  
CC screening new opioid ligands, and for studying mechanisms of  
CC opioid action, e.g. drug addiction.  
SQ Sequence 356 AA;  
  
Query Match 59.3%; Score 1683; DB 11; Length 356;  
Best Local Similarity 62.8%; Pred. No. 7.48e-148;  
Matches 213; Conservative 60; Mismatches 62; Indels 4; Gaps 4;  
  
Db 3 septglgndslcpqtgspsmvtaitalmaysivcvglgfnflmyviivrytkmktatn 62  
QY 36 SDSNGSVGSEDOQLESAHSIPAIPVITAVYSVVFVGLVGNLSLVMEVLIIRYTKMKTATN 95  
Db 63 lyifnlaladalatstlpfqsvnylmgtpfgtlilckivisidymnftsiftlctmsvd 122  
QY 96 xyifnlaladalavtttmpfqsavylmnswhfgdvlckivisidymnftsiftlctmsvd 155  
Db 123 ryiavchpvrkaldfrtprnakivncwllssaiqlpvmfmattkyrg-s-idcrltfs 180  
QY 156 ryiavchpvrkaldfrtprnakivncwllssaiqlpvmfmattkyrg-s-idcrltfs 215  
Db 181 hptw-ywenllkicvfifafimpvllitvcyglmllrlksvrmlsgskekdnlrritrm 239  
QY 216 DDEYSWMDLFMKICVFAFVPIVLIITVCTILMLRLKSVRLLSGSRKDRNLRRITKL 275  
Db 240 vlvvvavfivcwtpihivvikalilitpetftqtwshfciatgytncslnpvlyafide 299  
QY 276 vlvvvavfivcwtpihivvikalilitpetftqtwshfciatgytncslnpvlyafide 335  
Db 300 afkrctrefcipcststieqgnstrvrgntrehpstantv 338  
QY 336 NEKRCFRDCEPPIKMRMEROSTNVR-NTVQDPASMRDV 373

RESULT 7  
ID R71966 standard; Protein; 400 AA.  
AC R71966;  
DT 20-OCT-1995 (first entry)  
DE Human mu opioid receptor.  
KW Mu opioid receptor; MOR; gene therapy; diagnostic.  
OS Homo sapiens.  
PN WO9507983-A.  
PD 23-MAR-1995.  
PF 13-SEP-1994; U10358.  
PR 13-SEP-1993; US-120601.  
PA (INDV ) UNITV INDIANA FOUND.  
PI Yu L;  
DR WPI; 95-131351/17.  
DR N-PSDB; Q89226.  
PT New nucleic acid encoding new human mu opioid receptor - and  
PT related vectors, transformed cells, antibodies etc., useful in  
PT diagnosis, treatment and drug screening.  
PS Claim 4: Page 211-214; 266pp; English.  
CC A cDNA library constructed from human caudate nucleus mRNA was  
CC screened with rat mu opioid receptor cDNA under conditions of  
CC low stringency. One positive clone included the sequence given in  
CC Q89226, encoding a mu opioid receptor MOR (R71964). The cDNA  
CC is used for prodn. of recombinant MOR, in gene therapy, etc.  
SQ Sequence 400 AA;  
  
Query Match 59.1%; Score 1677; DB 13; Length 400;  
Best Local Similarity 66.6%; Pred. No. 2.86e-147;  
Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps 3;  
  
Db 70 altlmalsivcvglgfnflmyviivrytkmktatniyifnlaladalatstlpfqsvn 129  
QY 59 PVITAVYSVVFVGLVGNLSLVMEVLIIRYTKMKTATNITIFNLALADALVTTMPFQSAV 118  
Db 130 ylmgtwpgtlilckivisidymnftsiftlctmsvdryiavchpvrkaldfrtprnakil 189  
QY 119 ylmnswhfgdvlckivisidymnftsiftlctmsvdryiavchpvrkaldfrtprnakil 178  
Db 190 nvcnwllssaiqlpvmfmattkyrg-s-idcrltfshtw-ywenllkicvfifafimp 246  
QY 179 NCIWMLASSVGISAIIVLGTGKVRDYVIECSLQFPDEYSWMDLFMKICVFAFVPI 238  
Db 247 vllitvcyglmllrlksvrmlsgskekdnlrritrmvllvvavfivcwtpihivlika 306  
QY 239 VLIITVCTILMLRLKSVRLLSGSRKDRNLRRITKLVLVVAVFIICWTPIHIFILVEA 298  
Db 307 lvtipetftqtwshfciatgytncslnpvlyafidenfkrcfrefcipcststieqgnst 366  
QY 299 LGSTSHSTAALSSYFICIALGYTNSLNPLYAFIDENFKRCFRDCEPPIKMRMEROSTN 358  
Db 367 rirgntdrhps 377  
QY 359 RVRNTVQDPAS 369  
  
RESULT 8  
ID R76781 standard; Protein; 398 AA.  
AC R76781;  
DT 11-DEC-1995 (first entry)  
DE Rat mu opiate receptor.  
KW Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;  
KW drug abuse; analgesic.  
OS Rattus sp.  
PN WO9520667-A1.  
PD 03-AUG-1995.  
PF 30-JAN-1995; U01144.  
PR 28-JAN-1994; US-188275.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (USSH ) US SEC DEPT HEALTH.  
PI Johnson PS, Persico AM, Uhl G, Wang J;  
DR WPI; 95-275452/36.







Db 283 wtlivdinrrdplvvaalhlcialgyansslnpvlyafldenfkrcfrqlcrtpcgrqep 342  
QY 296 VEALGSTSHSTA-ALSSYYFCIALGYTNSLNPLYAFLDENFKRCFRDPCFPKRMER 354  
Db 343 gslrrprga 351  
QY 355 QSTNRRVNT 363

RESULT 13  
ID R48629 standard; Protein; 372 AA.  
AC R48629;  
DT 15-SEP-1994 (first entry)  
DE Sequence of murine delta opioid receptor deduced from the  
DE DOR-1 cDNA clone.  
KW Opioid receptor; morphine; opiate.  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT Region 46..75  
FT /label= putative membrane spanning region  
FT Region 85..102  
FT /label= see above  
FT Region 125..144  
FT /label= see above  
FT Region 168..189  
FT /label= see above  
FT Region 215..238  
FT /label= see above  
FT Region 262..284  
FT /label= see above  
FT Region 295..308  
FT /label= see above  
PN W09404552-A.  
PD 03-MAR-1994.  
PF 13-AUG-1993; U07665.  
PR 13-AUG-1992; US-929200.  
PA (REGC ) UNIV CALIFORNIA.  
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;  
DR WPI; 94-083099/10.  
DR N-PSDB; Q66700.  
PT DNA encoding opioid receptors and antibodies against this  
PT receptor - used to express and locate these receptors, and screen  
PT cpds. for opioid (ant)agonist activity  
PS Claim 10; Fig 5; 74pp; English.  
CC A cDNA library was constructed using mRNA isolated from the NG109-15  
CC cell line. A single clone, named the DOR-1 clone was isolated.  
CC Comparisons with known sequences in Genbank showed highest homology  
CC between DOR-1 and the G-protein-coupled somatostatin receptor. Other  
CC features of the DOR-1 clone AA sequence deduced from the cDNA  
CC sequence include 3 consensus glycosylation sites at residues 18 and  
CC 33 (predicted to be in the extracellular N-terminal domain), and at  
CC residue 310 (close to the C-terminus and predicted to be  
CC intracellular). Phosphokinase C consensus sites are present within  
CC predicted intracellular domains, at residues 242,255, 344 & 352.  
CC Seven putative membrane-spanning regions were identified. The DOR-1  
CC clone produces a delta receptor with a predicted mol. wt. of 40,558  
CC kdaltons prior to post-translational modifications.  
SQ Sequence 372 AA;

Query Match 56.3%; Score 1597; DB 9; Length 372;  
Best Local Similarity 66.7%; Pred. No. 1.64e-139;  
Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5;  
Db 47 alataitalysavcavglgnvlfmfgivrytklktatniyifnlaladalatstlpfgs 106  
QY 57 AIPVITAVYSVFEVGLVGNLSLVMFVIIRYTKMKTATNTIIFNLALADALVTTMPRQS 116  
Db 107 akylmetwpgfegllckavlsidymnftsiftltmmsvdyriavchpvpkaldfrtpakak 166  
QY 117 AVYLMNSWPFEGDVLCKIVISIDYYNMTSIFTLTMSVDRIYAVCHPVKALDFRTPAKAK 176  
Db 167 llniciwvlasgvvpinvmavtqprdga-vv-cmlgfpsp--swywdtvtckicvflfaf 222

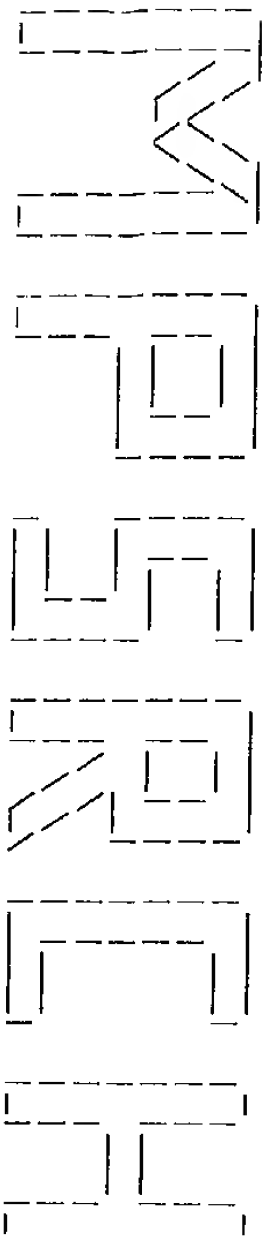
QY 177 IINICIWLLASSVGISAVLGGTKVREDVDYIECSLQFPDDEYSW-WDLFMKICVFVFAF 235  
Db 223 vvpilittvcyglmllrlsvrllsgskeksrslrritmvlvvvgafvwcwapihifvi 282  
QY 236 VIPVLIIVCYTLMILRLKSVRLLSGSRKDRNLRRITKLVVVAVFIICWTPIHIFIL 295  
Db 283 wtlivdinrrdplvvaalhlcialgyansslnpvlyafldenfkrcfrqlcrtpcgrqep 342  
QY 296 VEALGSTSHSTA-ALSSYYFCIALGYTNSLNPLYAFLDENFKRCFRDPCFPKRMER 354  
Db 343 gslrrprga 351  
QY 355 QSTNRRVNT 363

RESULT 14  
ID R66503 standard; Protein; 371 AA.  
AC R66503;  
DT 19-JAN-1995 (first entry)  
DE Murine delta opioid receptor.  
DE delta opioid; enkephalin; receptor; mouse; murine; analgesic; pain;  
KW drug addiction; neurological disorder; psychiatric; disorder;  
KW cardiovascular disorder.  
OS Mus musculus.  
PN FR2697850-A.  
PD 13-MAY-1994.  
PF 10-NOV-1992; 013526.  
PR 10-NOV-1992; FR-013526.  
PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.  
PI Kieffer B;  
DR WPI; 94-178255/22.  
DR N-PSDB; Q66656.  
PT New nucleic acid encoding opioid receptor - and related  
PT polypeptide, antisense nucleic acid, probes, recombinant cells  
PT and ligands, useful in diagnosis and treatment of e.g.  
PT neurological disorders  
PS Claim 8; Page 19-20; 29pp; French.  
CC A cDNA bank constructed from hybridoma NG108-15, was used to  
CC transfect COS-1 cells. The cells were tested for ability to bind  
CC tritium-labelled Tyr-D-Thr-Phe-Leu-Thr, in the presence or  
CC absence of the opioid antagonist naloxone. Clone K56 was isolated  
CC from a positive colony and found to contain a 2216bp insert. This  
CC cDNA encodes a delta opioid (enkephalin) receptor with apparent  
CC dissociation constant 1.4nM and Bmax 3.9-6.4 pmole/mg protein.  
SQ Sequence 371 AA;

Query Match 52.8%; Score 1499; DB 10; Length 371;  
Best Local Similarity 64.9%; Pred. No. 5.12e-130;  
Matches 200; Conservative 52; Mismatches 51; Indels 5; Gaps 5;  
Db 47 alataitalysavcavglgnvlfmfgivrytklktatniyifnlaladalatstlpfgs 106  
QY 57 AIPVITAVYSVFEVGLVGNLSLVMFVIIRYTKMKTATNTIIFNLALADALVTTMPRQS 116  
Db 107 akylmetwpgfegllckavlsidymnftsiftltmmsvdyriavchpvpkaldfrtpakak 166  
QY 117 AVYLMNSWPFEGDVLCKIVISIDYYNMTSIFTLTMSVDRIYAVCHPVKALDFRTPAKAK 176  
Db 167 llniciwvlasgvvpinvmavtn-pgmvgwacs-sspv-qlvl-dtvtckicvflfafv 222  
QY 177 IINICIWLLASSVGISAVLGGTKVREDVDYIECSLQFPDDEYSWMDLFMKICVFVFAFV 236  
Db 223 vvpilittvcyglmllrlsvrllsgskeksrslrritmvlvvvgafvwcwapihifvi 282  
QY 237 IPVLIIVCYTLMILRLKSVRLLSGSRKDRNLRRITKLVVVAVFIICWTPIHIFILV 296  
Db 283 wtlivdinrrdplvvaalhlcialgyansslnpvlyafldenfkrcfrqlcrtpcgrqep 342  
QY 297 EALGSTSHSTA-ALSSYYFCIALGYTNSLNPLYAFLDENFKRCFRDPCFPKRMERQ 355  
Db 343 slrrprga 350







Release 2.1D John F. Collins, Biocomputing Research Unit.  
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\*\*\*\*\*  
MSPrch\_pp Protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Aug 26 14:50:23 1997; MasPar time 18.98 Seconds

Tabular output not generated. 578.520 Million cell updates/sec

Title: >US-08-292-694A-2  
Description: (1-380) from US08292694A.pep  
Perfect Score: 2839  
Sequence: 1 MESPIQIFRGDPGPTCSPSA.....RNTVQDPASMRDVGGMKPV 380

Scoring table: PAM 150  
Gap 11

Searched: 91006 seqs, 28888923 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir51  
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3  
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8  
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 47.869; Variance 123.437; scale 0.388

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2839	100.0	380	14	A48227	kappa opiodid recepto	0.00e+00
2	2829	99.6	380	14	S36143	kappa opiodid recepto	0.00e+00
3	2816	99.2	380	14	JC2434	kappa-opiodid recepto	0.00e+00
4	2747	96.8	380	13	JC2338	kappa opiodid recepto	0.00e+00
5	2746	96.7	380	13	I57005	kappa opiodid recepto	0.00e+00
6	2610	91.9	380	14	A55259	kappa opiodid recepto	0.00e+00
7	1680	59.2	392	13	S65693	opioid receptor mu v	1.56e-244
8	1678	59.1	398	14	A57510	mu opiodid receptor -	3.32e-244
9	1677	59.1	400	13	I56553	opioid receptor mu -	4.84e-244
10	1676	59.0	398	14	S34593	mu opiate receptor mu -	7.06e-244
11	1674	58.4	398	14	I56517	mu-opioid receptor -	1.50e-243
12	1659	58.0	398	14	I56504	mu opiodid receptor -	4.31e-241
13	1612	56.8	372	13	I38657	delta opiate recepto	2.14e-233
14	1610	56.7	372	14	S34592	delta opiodid recepto	4.55e-233
15	1597	56.3	372	14	B48227	delta opiodid recepto	6.11e-231
16	1499	52.8	371	16	S36745	delta opiodid recepto	6.44e-215
17	1473	51.9	367	14	I56520	G protein-coupled re	1.13e-210
18	1471	51.8	357	14	I49122	orphan opiodid recept	2.40e-210
19	1471	51.8	367	14	JC2421	opioid receptor homo	2.40e-210
20	1470	51.8	367	14	I49022	K3 opiate receptor -	3.50e-210
21	1465	51.6	370	13	S43087	opioid receptor, ORL	2.29e-209

22	980	34.5	391	14	C41795	somatostatin recepto	9.64e-131
23	978	34.4	391	14	A39297	somatostatin recepto	2.02e-130
24	976	34.4	391	13	A41795	somatostatin recepto	4.23e-130
25	968	34.1	388	13	JN0605	somatostatin recepto	8.15e-129
26	963	33.9	384	14	A47249	brain-specific somat	5.18e-128
27	954	33.6	384	14	JC4629	somatostatin recepto	1.44e-126
28	936	33.0	369	14	JC2083	somatostatin recepto	1.11e-123
29	927	32.7	369	14	A45291	somatostatin recepto	3.07e-122
30	922	32.5	369	14	D41795	somatostatin recepto	1.94e-121
31	912	32.1	369	13	B41795	somatostatin recepto	7.75e-120
32	909	32.0	346	14	S29248	somatostatin recepto	2.34e-119
33	850	29.9	333	13	I38974	G protein-coupled re	6.25e-110
34	819	28.8	363	13	I57955	somatostatin recepto	5.43e-105
35	819	28.8	364	13	JN0763	somatostatin recepto	5.43e-105
36	815	28.7	418	13	A46226	somatostatin recepto	2.35e-104
37	792	27.9	328	13	I38973	G protein-coupled re	1.06e-100
38	788	27.8	363	14	I57940	somatostatin recepto	1.60e-100
39	734	25.9	428	14	S30508	probable G protein-c	1.65e-91
40	732	25.8	428	14	A44021	somatostatin recepto	3.42e-91
41	639	22.5	359	16	S44425	angiotensin II recep	1.46e-76
42	629	22.2	359	13	JC1104	angiotensin II recep	5.36e-75
43	623	21.9	355	13	A45177	chemokine (C-C) rece	4.64e-74
44	617	21.7	359	14	A48857	AT1 angiotensin II r	4.01e-73
45	616	21.7	359	16	S15403	angiotensin II recep	5.75e-73

ALIGNMENTS

RESULT 1  
ENTRY A48227 #type complete  
TITLE kappa opiodid receptor 1 - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 27-Oct-1995

ACCESSIONS  
REFERENCE A48227; JC4138  
#authors Yasuda, K.; Raynor, K.; Kong, H.; Breder, C.D.; Takeda, J.;  
#journal Reisine, T.; Bell, G.I.  
#title Proc. Natl. Acad. Sci. U.S.A. (1993) 90:6736-6740  
#accession Cloning and functional comparison of kappa and delta opiodid  
#title receptors from mouse brain.  
A48227

REFERENCE  
#authors Liu, H.C.; Lu, S.; Augustin, L.B.; Felsheim, R.F.; Chen,  
#journal H.C.; Loh, H.H.; Wei, L.N.  
#title Biochem. Biophys. Res. Commun. (1995) 209:639-647  
#accession Cloning and promoter mapping of mouse kappa opiodid receptor  
#title gene.  
JC4138

COMMENT This receptor exists in different areas of the central and  
peripheral nervous systems, and mediates many physiological and  
pharmacological effects of opiates and opiodid compounds.  
Glu  
The authors translated the codon CAG for residue 365 as

GENETICS  
#gene kor  
#keywords brain; G protein-coupled receptor; glycoprotein; opiodid  
#summary peptide; phosphoprotein; transmembrane protein  
#length 380 #molecular-weight 42652 #checksum 9937

QUERY MATCH  
Best Local Similarity 100.0%; Score 2839; DB 14; Length 380;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mespiqifrgdpgptcpspsacilpnssswfpnwaesdngsvgsedqglshispaipv 60  
QY 1 MESPIQIFRGDPGPTCSPSACLPSNSSFPPNWAESDSNGSVGSEDDQLSHISPAIPV 60

Db 61 itavysvfvvlgvgnslvmfvliirytkmktatniyifnlaladalvttmpfgsavyl 120  
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QY 61 IITAVYSVFEVVGVLGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTMPFQSAVYL 120  
Db 121 mmswpgdvclckivisidynnmtsifltlmsvdryiavchpvcakldfrtpklakini 180  
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QY 121 MNSWPFQDVCLCKIVISIDYNNMTSIFLTLMMSVDRIYAVCHPVKALDFRTPKLAKIINI 180  
Db 181 ciwllassvgisaivlggtkvredvdviecsiqfpddeyswdlfmkicvtfafvipvl 240  
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QY 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSIQFPDDEYSWMDLFMKICVFVFAFVIPVL 240  
Db 241 liivcytlmlrlksvrlslgsrekdrnlrrlrlklylvvavfllcwtpihlilvealg 300  
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QY 241 IIVCYTLMILRLKSVRLSLGSREKDRNLRRITKLVLVAVFIIICWTPIHILVEALG 300  
Db 301 stshstaalssyfcialgytnslnpvlyafldenfkrcfrdfcfpikmmergstnrv 360  
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QY 301 STSHSTAALSSYFCIALGYTNSLNPVLYAFLDENFKRCFRDFCFPIKMERGSTNRV 360  
Db 361 rntvqdpasmrdvvgmnpv 380  
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QY 361 RNTVQDPASMRDVGGMNKPV 380

RESULT 2  
ENTRY 2  
TITLE kappa opiod receptor - rat  
ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 10-Dec-1993 #sequence\_revision 19-Oct-1995 #text\_change 06-Sep-1996

ACCESSIONS  
REFERENCE  
#authors Nishi, M.; Takeshima, H.; Fukuda, K.; Kato, S.; Mori, K.  
#journal FEBS Lett. (1993) 330:77-80  
#title cDNA cloning and pharmacological characterization of an opiod receptor with high affinities for kappa-subtype-selective ligands.  
#accession S36143  
#status preliminary  
#molecule\_type mRNA  
#residues 1-380 #label NIS

REFERENCE  
#authors Chen, Y.; Mestek, A.; Liu, J.; Yu, L.  
#journal Biochem. J. (1993) 295:625-628  
#title Molecular cloning of a rat kappa opiod receptor reveals sequence similarities to the mu and delta opiod receptors.  
#accession S38825  
#status preliminary  
#molecule\_type mRNA  
#residues 1-380 #label CHE  
#cross-references GB:L22001

REFERENCE  
#authors Minami, M.; Toya, T.; Katao, Y.; Maekawa, K.; Nakamura, S.; Onogi, T.; Kaneko, S.; Satoh, M.  
#journal FEBS Lett. (1993) 329:291-295  
#title Cloning and expression of a cDNA for the rat kappa-opiod receptor.  
#accession S36102  
#molecule\_type mRNA  
#residues 1-41, 'L', 43-380 #label MIN

REFERENCE  
#authors Li, S.; Zhu, J.; Chen, C.; Chen, Y.W.; Deriel, J.K.; Ashby, B.; Liu-Chen, L.Y.  
#journal Biochem. J. (1993) 295:629-633  
#title Molecular cloning and expression of a rat kappa opiod receptor.  
#accession S39015  
#molecule\_type mRNA  
#residues 1-344, 'Y', 346-380 #label LIS

REFERENCE  
#authors Meng, F.; Xie, G.

#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9954-9958  
#title Cloning and pharmacological characterization of a rat kappa opiod receptor.  
#cross-references MUID:94052210  
#accession A48789  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type mRNA  
#residues 1-380 #label RES  
#cross-references EMBL:U00442; NID:g403486; CDS\_PID:g403487  
SUMMARY #length 380 #molecular-weight 42688 #checksum 9972

Query Match 99.6%; Score 2829; DB 14; Length 380;  
Best Local Similarity 98.9%; Pred. No. 0.00e+00;  
Matches 376; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 mespiqlfrgdpptcspascllpnsswfpnwaesdsgsvsgedqqlsahispaiyv 60  
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QY 1 MESPIQIFRGDPPTCSPSACLLPNSSSWFPNWAESDSNGSVSGEDQQLSAHISPAIV 60  
Db 61 itavysvfvvlgvgnslvmfvliirytkmktatniyifnlaladalvttmpfgsavyl 120  
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QY 61 IITAVYSVFEVVGVLGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTMPFQSAVYL 120  
Db 121 mmswpgdvclckivisidynnmtsifltlmsvdryiavchpvcakldfrtpklakini 180  
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QY 121 MNSWPFQDVCLCKIVISIDYNNMTSIFLTLMMSVDRIYAVCHPVKALDFRTPKLAKIINI 180  
Db 181 ciwllassvgisaivlggtkvredvdviecsiqfpddeyswdlfmkicvtfafvipvl 240  
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QY 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSIQFPDDEYSWMDLFMKICVFVFAFVIPVL 240  
Db 241 liivcytlmlrlksvrlslgsrekdrnlrrlrlklylvvavfllcwtpihlilvealg 300  
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QY 241 IIVCYTLMILRLKSVRLSLGSREKDRNLRRITKLVLVAVFIIICWTPIHILVEALG 300  
Db 301 stshstaalssyfcialgytnslnpvlyafldenfkrcfrdfcfpikmmergstnrv 360  
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QY 301 STSHSTAALSSYFCIALGYTNSLNPVLYAFLDENFKRCFRDFCFPIKMERGSTNRV 360  
Db 361 rntvqdpasmrdvvgmnpv 380  
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QY 361 RNTVQDPASMRDVGGMNKPV 380

RESULT 3  
ENTRY 3  
TITLE JC2434 #type complete  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 21-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 05-Apr-1995

ACCESSIONS  
REFERENCE  
#authors Nishi, M.; Takeshima, H.; Mori, M.; Nakagawara, K.; Takeuchi, T.  
#journal Biochem. Biophys. Res. Commun. (1994) 205:1353-1357  
#title Structure and chromosomal mapping of genes for the mouse kappa-opiod receptor and an opiod receptor homologue (MOR-C).  
#accession JC2434  
#molecule\_type mRNA  
#residues 1-380 #label NIS  
#cross-references DDBJ:D31663

GENETICS  
#map\_position 1A2-3  
#introns 86/2; 204/1  
KEYWORDS receptor  
SUMMARY #length 380 #molecular-weight 42630 #checksum 9705

Query Match 99.2%; Score 2816; DB 14; Length 380;  
Best Local Similarity 99.5%; Pred. No. 0.00e+00;  
Matches 378; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 mespiqlfrgdpptcspascllpnsswfpnwaesdsgsvsgedqqlsahispaiyv 60

QY 1 MESPIQIFRGDGPFTCSPSACLPPNSSSWFPNWAESDSNGSVGSEDDQLESAAHISPAIPV 60  
Db 61 IITAVSVYFVVGVLVGNLSVMFVILIRYTKMKTATNIYIFNLALADALVTTMPFGSAVYL 120  
QY 61 IITAVSVYFVVGVLVGNLSVMFVILIRYTKMKTATNIYIFNLALADALVTTMPFGSAVYL 120  
Db 121 mswpfgdvLckivisiDyymftsiflTmmsvdryIavchpYkaldfrtPlkakiNI 180  
QY 121 MNSWPFGBVLCkIVISIDYNNMFTSIFLTmMSVDRIYAVCHPYKALDERTPlkAKIINI 180  
Db 181 ciwllassvgisaivlggtkvredvdiECslQFPDDEYSWMDLFMKICVFVFAFVIPVL 240  
QY 181 CIWLLASSVGISAIVLGGTKVREDVDYIECSLQFPDDEYSWMDLFMKICVFVFAFVIPVL 240  
Db 241 IIVCYTLMILRLKSVRLSGSREKDRNLRRITKLVVAVAFIICWTPIHIFILVEALG 300  
QY 241 IIVCYTLMILRLKSVRLSGSREKDRNLRRITKLVVAVAFIICWTPIHIFILVEALG 300  
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QY 301 STSHSTAALSSYYFCIALGYTNSLNPLVLYAFLDENFKRCFRDFCFPIKRMERQSTNRV 360  
Db 361 rntvqdpasmrdvYgmnkPv 380  
QY 361 RNTYQDPASMRDVYGMNKPV 380

RESULT 4  
ENTRY JC2338 #type complete  
TITLE kappa opioid receptor - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 05-Jan-1996

ACCESSIONS JC2338; A55354  
REFERENCE JC2338  
#authors Mansson, E.; Bare, L.; Yang, D.  
#journal Biochem. Biophys. Res. Commun. (1994) 202:1431-1437  
#title Isolation of a human kappa opioid receptor cDNA from placenta.

#accession JC2338  
#molecule\_type mRNA  
#residues 1-380 #label MAN  
#experimental\_source placenta  
REFERENCE A55354  
#authors Wang, J.B.; Johnson, P.S.; Wu, J.M.; Wang, W.F.; Uhl, G.R.  
#journal J. Biol. Chem. (1994) 269:25966-25969  
#title Human kappa opiate receptor second extracellular loop elevates dynorphin's affinity for human mu/kappa chimeras.

#accession A55354  
#status preliminary  
#molecule\_type mRNA  
#residues 136-279 #label WAN  
COMMENT ##cross-references GB:L36130  
KEYWORDS This receptor preferentially binds to dynorphins.  
FEATURE receptor; transmembrane protein  
60-85 #domain transmembrane #status predicted #label TM1\  
95-114 #domain transmembrane #status predicted #label TM2\  
133-154 #domain transmembrane #status predicted #label TM3\  
177-199 #domain transmembrane #status predicted #label TM4\  
228-251 #domain transmembrane #status predicted #label TM5\  
275-296 #domain transmembrane #status predicted #label TM6\  
311-333 #domain transmembrane #status predicted #label TM7  
SUMMARY #length 380 #molecular-weight 42659 #checksum 8304

Query Match 96.8%; Score 2747; DB 13; Length 380;  
Best Local Similarity 93.9%; Pred. No. 0.00e+00;  
Matches 357; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

Db 1 mespiqifrgpgptcaspacLppnssawfpYgaepdngsagsedaqlepahispaipv 60  
QY 1 MESPIQIFRGDGPFTCSPSACLPPNSSSWFPNWAESDSNGSVGSEDDQLESAAHISPAIPV 60

Db 61 IITAVSVYFVVGVLVGNLSVMFVILIRYTKMKTATNIYIFNLALADALVTTMPFGSTVYL 120  
QY 61 IITAVSVYFVVGVLVGNLSVMFVILIRYTKMKTATNIYIFNLALADALVTTMPFGSAVYL 120  
Db 121 mswpfgdvLckivisiDyymftsiflTmmsvdryIavchpYkaldfrtPlkakiNI 180  
QY 121 MNSWPFGBVLCkIVISIDYNNMFTSIFLTmMSVDRIYAVCHPYKALDERTPlkAKIINI 180  
Db 181 ciwllassvgisaivlggtkvredvdiECslQFPDDEYSWMDLFMKICVFVFAFVIPVL 240  
QY 181 CIWLLASSVGISAIVLGGTKVREDVDYIECSLQFPDDEYSWMDLFMKICVFVFAFVIPVL 240  
Db 241 IIVCYTLMILRLKSVRLSGSREKDRNLRRITKLVVAVAFIICWTPIHIFILVEALG 300  
QY 241 IIVCYTLMILRLKSVRLSGSREKDRNLRRITKLVVAVAFIICWTPIHIFILVEALG 300  
Db 301 stshstaalssyyfciAlgytnsslnpVlyafldenfkrcfrdcfPlkmmergstsrY 360  
QY 301 STSHSTAALSSYYFCIALGYTNSLNPLVLYAFLDENFKRCFRDFCFPIKRMERQSTNRV 360  
Db 361 rntvqdpaylrIdidgmNkPv 380  
QY 361 RNTYQDPASMRDVYGMNKPV 380

RESULT 5  
ENTRY I57005 #type complete  
TITLE kappa opioid receptor - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 02-Jul-1996

ACCESSIONS I57005  
REFERENCE I57005  
#authors Zhu, J.; Chen, C.; Xue, J.  
#journal Life Sci. (1995) 56:201-207  
#title Cloning of a human .kappa. opioid receptor from the brain.

#accession I57005  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type mRNA  
#residues 1-380 #label RES  
#cross-references GB:L37362; MID:g722617; CDS\_PID:g722618

GENETICS  
#note gene name OPRK1  
SUMMARY #length 380 #molecular-weight 42645 #checksum 8302

Query Match 96.7%; Score 2746; DB 13; Length 380;  
Best Local Similarity 93.7%; Pred. No. 0.00e+00;  
Matches 356; Conservative 18; Mismatches 6; Indels 0; Gaps 0;

Db 1 mdspiqifrgpgptcaspacLppnssawfpYgaepdngsagsedaqlepahispaipv 60  
QY 1 MESPIQIFRGDGPFTCSPSACLPPNSSSWFPNWAESDSNGSVGSEDDQLESAAHISPAIPV 60  
Db 61 IITAVSVYFVVGVLVGNLSVMFVILIRYTKMKTATNIYIFNLALADALVTTMPFGSTVYL 120  
QY 61 IITAVSVYFVVGVLVGNLSVMFVILIRYTKMKTATNIYIFNLALADALVTTMPFGSAVYL 120  
Db 121 mswpfgdvLckivisiDyymftsiflTmmsvdryIavchpYkaldfrtPlkakiNI 180  
QY 121 MNSWPFGBVLCkIVISIDYNNMFTSIFLTmMSVDRIYAVCHPYKALDERTPlkAKIINI 180  
Db 181 ciwllassvgisaivlggtkvredvdiECslQFPDDEYSWMDLFMKICVFVFAFVIPVL 240  
QY 181 CIWLLASSVGISAIVLGGTKVREDVDYIECSLQFPDDEYSWMDLFMKICVFVFAFVIPVL 240  
Db 241 IIVCYTLMILRLKSVRLSGSREKDRNLRRITKLVVAVAFIICWTPIHIFILVEALG 300  
QY 241 IIVCYTLMILRLKSVRLSGSREKDRNLRRITKLVVAVAFIICWTPIHIFILVEALG 300  
Db 301 stshstaalssyyfciAlgytnsslnpVlyafldenfkrcfrdcfPlkmmergstsrY 360  
QY 301 STSHSTAALSSYYFCIALGYTNSLNPLVLYAFLDENFKRCFRDFCFPIKRMERQSTNRV 360

Db 361 :ntvqdpaylrdidgmkp 380  
QY 361 :NTVQDPASMRDVGGMNKP 380

RESULT 5  
ENTRY A55259 #type complete  
TITLE kappa opioid receptor - guinea pig  
ALTERNATE\_NAMES dynorphin receptor  
ORGANISM #formal\_name Cavia porcellus #common\_name guinea pig  
DATE 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 06-Feb-1995

ACCESSIONS A55259  
REFERENCE A55259  
#authors Xie, G.; Meng, F.; Mansour, A.; Thompson, R.C.; Hoversten, M.T.; Goldstein, A.; Watson, S.J.; Akil, H.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:3779-3783  
#title Primary structure and functional expression of a guinea pig kappa opioid (dynorphin) receptor.  
#accession A55259  
##status preliminary  
##molecule\_type mRNA  
##residues 1-380 #label XIE  
##cross-references GB:U04092

KEYWORDS transmembrane protein  
SUMMARY #length 380 #molecular-weight 42736 #checksum 7081

Query Match 91.9%; Score 2610; DB 14; Length 380;  
Best Local Similarity 92.9%; Pred. No. 0.00e+00;  
Matches 338; Conservative 21; Mismatches 5; Indels 0; Gaps 0;

Db 17 :arnacllpnsgawlpgwaepdngnsagpqdeglepahispaipvilitavysvfvvglyg 76  
QY 17 :SPSACLLPNSSSWFPNMAESDNGSVGSEDQQLSAHISPAIPVILITAVYSVFEVGLVG 76  
Db 77 :nslvmfvilrlytkmktatnlyifnlaladalvtttmpfgstvylnmswpfgdvicklvis 136  
QY 77 :NSLVMFVIIRYTKMTATNITIFNLALADALVTITMPFGSAVYILNMSWPFSGDVLCKIYIS 136  
Db 137 :ldyyumftsifltmmsvdryiaavchpvkaldfrtplkakliniciwllssvgisail 196  
QY 137 :IDYYNMFTSIFLTMMSSVDRYIAVCHPVKALDERTPLKAKIINICIWLLASSVGISAILVL 196  
Db 197 :ggtkvrredvdielsqlfpddyswdfimkicvfvafvipyvliivcytlmilrlkev 256  
QY 197 :GGTKVRREDVDVIECSLQFPDDEYSWDFIMKICVFVFAFVPIVLIIVCYTLMILRLKSV 256  
Db 257 :rlsgsrekdrnlrrlrlvlyvvaafficwtpihifilvealgstshstaalssyyfci 316  
QY 257 :RLSGSREKDRNLRRITKLVLVVAFFIICWTPIHIFILVEALGSTSHSTAALSSYYFCI 316  
Db 317 :algytnsslnpilyafidenfkrcfrdcfpikmmergqstsrvtvqdpaymrnvdy 376  
QY 317 :ALGYTNSSLNPLYAFIDENFKRCFRDCFPKMRMERQSTNRVNTVQDPASMRDVGGM 376  
Db 377 :nkpv 380  
QY 377 :NKPV 380

RESULT 7  
ENTRY S65693 #type complete  
TITLE opioid receptor mu variant MOR1A - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 12-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 26-Jul-1996

ACCESSIONS S65693  
REFERENCE S65693  
#authors Bare, L.A.; Mansson, E.; Yang, D.  
#submission Submitted to the EMBL Data Library, July 1994  
#description Expression of two variants of the human mu opioid receptor mRNA in SK-N-SH cells and human brain.

#accession S65693  
##molecule\_type mRNA  
##residues 1-392 #label BAR  
##cross-references EMBL:U12569

REFERENCE S51215  
#authors Bare, L.A.; Mansson, E.; Yang, D.  
#journal FEBS Lett. (1994) 354:213-216  
#title Expression of two variants of the human mu opioid receptor mRNA in SK-N-SH cells and human brain.  
#accession S51216  
##molecule\_type mRNA  
##residues 387-392 #label BAR  
SUMMARY #length 392 #molecular-weight 43939 #checksum 6977

Query Match 59.2%; Score 1680; DB 13; Length 392;  
Best Local Similarity 65.0%; Pred. No. 1.56e-244;  
Matches 210; Conservative 53; Mismatches 56; Indels 4; Gaps 4;

Db 70 :aitmalysivcvgvlfgnflvmyvivrytkmktatnlyifnlaladalstlpfgsv 129  
QY 59 :PVILITAVYSVFEVGLVGNLSLVMFVIIRYTKMTATNITIFNLALADALVTITMPFGSAV 118  
Db 130 :ylmgtpfgtllickivsidyymftsifltcmsvdryiaavchpvkaldfrtprnakii 189  
QY 119 :YLMNSWPFGDVLCKIYISIDYNNMFTSIFLTMMSSVDRYIAVCHPVKALDERTPLKAKII 178  
Db 190 :nvcnwllsaiqlpymfiatttkyrqg-s-ldccltfshtw-ywenlkicvfifafimp 246  
QY 179 :NICIWLLASSVGISALVIGGTVKREDVDVIECSLQFPDDEYSWMDLFMKICVEFAFVLP 238  
Db 247 :vlitvcyglmrlrksvmlsgskedrnrlrrlrmvlyvvaavfivcwtpihlyvlika 306  
QY 239 :VLIIVCYTLMILRLKSVRLISGSREKDRNLRRITKLVLVVAFFIICWTPIHIFILVEA 298  
Db 307 :lvtipettfgtvswhficialgytnsclnplyafidenfkrcfrefciptsnieqnst 366  
QY 299 :IGSTSHSTAALSSYYFCIALGYTNSSLNPLYAFIDENFKRCFRDCFPKMRMEROSTN 358  
Db 367 :rlrqnrthpstantvdrtnhqv 389  
QY 359 :RYRNTVQD-PASMRDVGGMNKP 380

RESULT 8  
ENTRY A57510 #type complete  
TITLE mu opioid receptor - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 08-Dec-1995 #sequence\_revision 08-Dec-1995 #text\_change 15-Oct-1996

ACCESSIONS A57510; I48665; I49300  
REFERENCE A57510  
#authors Kaufman, D.L.; Keith Jr., D.E.; Anton, B.; Tian, J.; Magendzo, K.; Newman, D.; Tran, T.H.; Lee, D.S.; Wen, C.; Xia, Y.R.; Lusis, A.J.; Evans, C.J.  
#journal J. Biol. Chem. (1995) 270:15877-15883  
#title Characterization of the murine mu opioid receptor gene.  
#accession A57510  
##status nucleic acid sequence not shown  
##molecule\_type mRNA  
##residues 1-398 #label KAU  
##cross-references GB:U19380

REFERENCE I48665  
#authors Min, B.H.; Augustin, L.B.; Felsheim, R.F.; Fuchs, J.A.; Loh, H.H.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:9081-9085  
#title Genomic structure analysis of promoter sequence of a mouse mu opioid receptor gene.  
#cross-references MUID:94377496  
#accession I48665  
##status translated from GB/EMBL/DBJ  
##molecule\_type DNA  
##residues 1-398 #label RES  
##cross-references EMBL:U10561; NID:g555696; CDS\_PID:g565069



```
REFERENCE I49300
#authors Rossi, G.C.; Pan, Y.X.; Brown, G.P.; Pasternak, G.W.
#journal FEBS Lett. (1995) 369:192-196
#title Antisense mapping the MOR-1 opioid receptor: evidence for
alternative splicing and a novel morphine-6
beta-glucuronide receptor.
#cross-references MUID:95377399
#accession I49300
#status nucleic acid sequence not shown; translation not shown;
translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-398 #label RE2
#cross-references EMBL:U26915; NID:g1055230; CDS_PID:g1055231
GENETICS
#introns 95/2; 213/1; 386/3
#note gene name MOR
KEYWORDS alternative splicing; G protein-coupled receptor;
glycoprotein; transmembrane protein
SUMMARY #length 398 #molecular-weight 44421 #checksum 8164
Query Match 59.1%; Score 1678; DB 14; Length 398;
Best Local Similarity 65.8%; Pred. No. 3.32e-244;
Matches 208; Conservative 55; Mismatches 49; Indels 4; Gaps 4;
Db 68 altimalysivcvgglfgnflvmyvivrytkmktatniyifnlaladalatlslpfgsvn 127
QY 59 PVITAVYSVVFVGVGLVGNLSVMFEVIRYTKMTATNIYIFNLALADALVTTMPFQSAV 118
Db 128 ylmgtwpgfnilckivisidymnftsiftlctmsvdryiavchpvcaldftprnakiv 187
QY 119 YLMSWPFQDVLCKIVISIDYNNMFTSFTLLTMSVDRIYAVCHPVCALDFRTPPLKAKII 178
Db 188 nvcnwilssaisglpvmfmatkkyrg-s-idcltfshtw-ywenllkicvffafimp 244
QY 179 NICIWLASSVGSISAVLGGTKVREDVDVIECSLQFPDDEYSWMDLFMKICVFVFAFVIP 238
Db 245 vlitvcyglmilrlksvrmllsgskekdnlrritrmvllvvavfivcwtphiyvika 304
QY 239 VLIIVCYTLMILRLKSVRLLSGSRKDRNLRLTKLVVVAVFTICWTPIHIFILVEA 298
Db 305 lvtipettfgtvswhfciaglytncslpnyafldenfkrcfrefciptsstieqnea 364
QY 299 LGSTSHSTAALSSYFCIALGYTNSLNPLYAFLDENFKRCFRDFCFPIKMRMEROSTN 358
Db 365 rirgntrehpsstantv 380
QY 359 RVR-NTVQDPASMRDV 373
RESULT 9
ENTRY I56553 #type complete
TITLE opiate receptor mu - human
ALTERNATE_NAMES MOR1 protein; opioid receptor mu
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
06-Sep-1996
ACCESSIONS I56553; A38991; S41075; S51215
REFERENCE I56553
#authors Mestek, A.; Hurley, J.H.; Bye, L.S.; Campbell, A.D.; Chen,
Y.; Tian, M.; Liu, J.; Schulman, H.; Yu, L.
#journal J. Neurosci. (1995) 15:2396-2406
#title The human mu opioid receptor: modulation of functional
desensitization by calcium/calmodulin-dependent protein
kinase and protein kinase C.
#cross-references MUID:95198115
#accession I56553
#status nucleic acid sequence not shown; translated from
GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-400 #label RES
#cross-references GB:L29301; NID:g459831; CDS_PID:g459832
REFERENCE A38991
#authors Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.;
```

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Griffin, C.A.; Uhl, G.R.
#submission submitted to GenBank, August 1994
#accession A38991
#status translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-50, 'N', 52-233, 'V', 235-400 #label WAN
#cross-references GB:L25119; CDS_PID:g452073
REFERENCE S41075
#authors Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.;
Griffin, C.A.; Uhl, G.R.
#journal FEBS Lett. (1994) 338:217-222
#title Human mu opiate receptor. cDNA and genomic clones,
pharmacologic characterization and chromosomal assignment.
#accession S41075
#status nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-50, 'N', 52-400 #label WA2
REFERENCE S51215
#authors Bare, L.A.; Mansson, E.; Yang, D.
#journal FEBS Lett. (1994) 354:213-216
#title Expression of two variants of the human mu opioid receptor
mRNA in SK-N-SH cells and human brain.
#accession S51215
#status preliminary
#molecule_type mRNA
#residues 387-400 #label BAR
GENETICS
#gene GDB:OPRML
#cross-references GDB:137216
#map_position 6q24-6q25
KEYWORDS G protein-coupled receptor; glycoprotein; transmembrane
protein
FEATURE
73-96 #domain transmembrane #label TM1\
107-132 #domain transmembrane #label TM2\
144-165 #domain transmembrane #label TM3\
188-208 #domain transmembrane #label TM4\
236-257 #domain transmembrane #label TM5\
283-304 #domain transmembrane #label TM6\
323-342 #domain transmembrane #label TM7\
9,12,33,40,48 #binding_site carbohydrate (Asn) (covalent) #status
predicted
SUMMARY #length 400 #molecular-weight 44779 #checksum 3741
Query Match 59.1%; Score 1677; DB 13; Length 400;
Best Local Similarity 66.6%; Pred. No. 4.84e-244;
Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps 3;
Db 70 altimalysivcvgglfgnflvmyvivrytkmktatniyifnlaladalatlslpfgsvn 129
QY 59 PVITAVYSVVFVGVGLVGNLSVMFEVIRYTKMTATNIYIFNLALADALVTTMPFQSAV 118
Db 130 ylmgtwpgfnilckivisidymnftsiftlctmsvdryiavchpvcaldftprnakii 189
QY 119 YLMSWPFQDVLCKIVISIDYNNMFTSFTLLTMSVDRIYAVCHPVCALDFRTPPLKAKII 178
Db 190 nvcnwilssaisglpvmfmatkkyrg-s-idcltfshtw-ywenllkicvffafimp 246
QY 179 NICIWLASSVGSISAVLGGTKVREDVDVIECSLQFPDDEYSWMDLFMKICVFVFAFVIP 238
Db 247 vlitvcyglmilrlksvrmllsgskekdnlrritrmvllvvavfivcwtphiyvika 306
QY 239 VLIIVCYTLMILRLKSVRLLSGSRKDRNLRLTKLVVVAVFTICWTPIHIFILVEA 298
Db 307 lvtipettfgtvswhfciaglytncslpnyafldenfkrcfrefciptsstieqnea 366
QY 299 LGSTSHSTAALSSYFCIALGYTNSLNPLYAFLDENFKRCFRDFCFPIKMRMEROSTN 358
Db 367 rirgntrehps 377
QY 359 RVRNTVQDPAS 369
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RESULT 10

ENTRY S34593 #type complete

TITLE mu opiate receptor - rat

ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat

DATE 10-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 06-Sep-1996

ACCESSIONS S34593; A48799; I58154

REFERENCE S34592

#authors Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.

#journal FEBS Lett. (1993) 327:311-314

#title Primary structures and expression from cDNAs of rat opioid receptor delta- and mu-subtypes.

#accession S34593

#molecule\_type mRNA

#residues 1-398 #label FUK

REFERENCE A48799

#authors Wang, J.

#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10230-10234

#title Mu opiate receptor: cDNA cloning and expression.

#cross-references MUID:94052137

#accession A48799

#status preliminary; translated from GB/EMBL/DBJ

#molecule\_type mRNA

#residues 1-398 #label WAN

#cross-references GB:L20684; NID:g409149; CDS\_PID:g409150

REFERENCE I58154

#authors Thompson, R.C.; Mansour, A.; Akil, H.; Watson, S.J.

#journal Neuron (1993) 11:903-913

#title Cloning and pharmacological characterization of a rat mu opioid receptor.

#cross-references MUID:94059560

#accession I58154

#status preliminary; translated from GB/EMBL/DBJ

#molecule\_type mRNA

#residues 1-398 #label THO

#cross-references GB:L22455; NID:g437671; CDS\_PID:g437672

GENETICS

#gene MUCR1

SUMMARY #length 398 #molecular-weight 44494 #checksum 8595

Query Match 59.0%; Score 1676; DB 14; Length 398;

Best Local Similarity 66.1%; Pred. No. 7.06e-244;

Matches 209; Conservative 53; Mismatches 50; Indels 4; Gaps 4;

Db 68 altimalysivcvvglfgnflvmvviivrytkmktatniyifnlaladalatstlpfgsvn 127

QY 59 PVIITAVYSVVEVVGIVGNSLVMEVILIRYTKMKTATNIYIFNLALADALVTTTMPFQSAV 118

Db 128 ylmgtwpgtllckivisiidynmftsiftlctmsvdryiavchpvcakldfrtprnakiv 187

QY 119 YLMNSWPFQDYLCIKIVISIDYNNFTSIFILTMMSVDRIYAVCHPVKALDFRTPLKAKII 178

Db 188 nvcnwllssaiglpvmfmattkkyrg-s-idctltfshptw-ywenllkicvfifafimp 244

QY 179 NTCIWLASSVGSISAIVLGGTKVREDVDVIECSIQFPDDEYSWMDLFMKICVFVFAFVIP 238

Db 245 vllitvcyglmllrksvrmllsgskednrlrritmvlvvaavfiavcwtpihiyvlika 304

QY 239 VLIITVCYTLMLRLKSVRLLSGSREKDRNLRRITKLVLVVAVFIIICWTPIHIFILVEA 298

Db 305 lltipetftqswfhcialgytnsclnpvlafidenfkrcfrefcipcsttieqgnst 364

QY 299 LGSTSHSTAALSSYYFCIALGYTNSSLNPVLYAFIDENFKRCFRCFPIKRMERQSTN 358

Db 365 rvrqntrehpstantv 380

QY 359 RVR-NTVQDPASMRDV 373

RESULT 11

ENTRY I56517 #type complete

TITLE mu-opioid receptor - rat

ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat

DATE 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 06-Sep-1996

ACCESSIONS I56517; I57951

REFERENCE I56517

#authors Bunzow, J.R.; Zhang, G.; Bouvier, C.; Saez, C.; Ronnekleiv, O.K.; Kelly, M.J.; Grandy, D.K.

#journal J. Neurochem. (1995) 64:14-24

#title Characterization and distribution of a cloned rat mu-opioid receptor.

#cross-references MUID:95096825

#accession I56517

#status preliminary; translated from GB/EMBL/DBJ

#molecule\_type mRNA

#residues 1-398 #label RES

#cross-references EMBL:U02083; NID:g403573; CDS\_PID:g403574

REFERENCE I57951

#authors Chen, Y.; Westek, A.; Liu, J.; Hurley, J.A.; Yu, L.

#journal Mol. Pharmacol. (1993) 44:8-12

#title Molecular cloning and functional expression of a mu-opioid receptor from rat brain.

#cross-references MUID:93341493

#accession I57951

#status preliminary; translated from GB/EMBL/DBJ

#molecule\_type mRNA

#residues 1-398 #label RE2

#cross-references GB:L13069; NID:g348250; CDS\_PID:g348251

SUMMARY #length 398 #molecular-weight 44508 #checksum 8374

Query Match 59.0%; Score 1674; DB 14; Length 398;

Best Local Similarity 65.8%; Pred. No. 1.50e-243;

Matches 208; Conservative 54; Mismatches 50; Indels 4; Gaps 4;

Db 68 altimalysivcvvglfgnflvmvviivrytkmktatniyifnlaladalatstlpfgsvn 127

QY 59 PVIITAVYSVVEVVGIVGNSLVMEVILIRYTKMKTATNIYIFNLALADALVTTTMPFQSAV 118

Db 128 ylmgtwpgtllckivisiidynmftsiftlctmsvdryiavchpvcakldfrtprnakiv 187

QY 119 YLMNSWPFQDYLCIKIVISIDYNNFTSIFILTMMSVDRIYAVCHPVKALDFRTPLKAKII 178

Db 188 nvcnwllssaiglpvmfmattkkyrg-s-idctltfshptw-ywenllkicvfifafimp 244

QY 179 NTCIWLASSVGSISAIVLGGTKVREDVDVIECSIQFPDDEYSWMDLFMKICVFVFAFVIP 238

Db 245 lllitvcyglmllrksvrmllsgskednrlrritmvlvvaavfiavcwtpihiyvlika 304

QY 239 VLIITVCYTLMLRLKSVRLLSGSREKDRNLRRITKLVLVVAVFIIICWTPIHIFILVEA 298

Db 305 lltipetftqswfhcialgytnsclnpvlafidenfkrcfrefcipcsttieqgnst 364

QY 299 LGSTSHSTAALSSYYFCIALGYTNSSLNPVLYAFIDENFKRCFRCFPIKRMERQSTN 358

Db 365 rvrqntrehpstantv 380

QY 359 RVR-NTVQDPASMRDV 373

RESULT 12

ENTRY I56504 #type complete

TITLE mu opioid receptor - rat

ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat

DATE 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 26-Jul-1996

ACCESSIONS I56504

REFERENCE I56504

#authors Zastawny, R.L.; George, S.R.; Nguyen, T.; Cheng, R.; Tsatsos, J.; Briones-Urbina, R.; O'Dowd, B.F.

#journal J. Neurochem. (1994) 62:2099-2105

#title Cloning, characterization, and distribution of a mu-opioid receptor in rat brain.

#cross-references MUID:94246380

#accession I56504

#status preliminary; translated from GB/EMBL/DBJ

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##molecule_type mRNA
##residues      1-398  ##label RES
##cross-references EMBL:U035424; NID:g1017731; CDS_PID:g1017732
SUMMARY          #length 398  #molecular-weight 44403  #checksum 8604

Query Match               58.4%; Score 1659; DB 14; Length 398;
Best Local Similarity    65.8%; Pred. No. 4.31e-241;
Matches     208; Conservative   53; Mismatches    51; Indels     4; Gaps     4

Db       68  aitimalysivcvglgfnflvmyviyrckmkatniyifnlaladalstlpfgsvn 127
        ::|::||| | |||::|||::|||::|||::|||::|||::|||::|||::|||
QY       59  PVITAVSVVFVGVGLGNSLMFVIIRYTKMTAINTIYNFLALADALTTPFQSAAV 118
        ylmgtwpgftllckivisidyymftsiftctmsvdryiaavchpvkaldfrprnakiv 187
Db       128  ylmgtwpgftllckivisidyymftsiftctmsvdryiaavchpvkaldfrprnakiv 187
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY       119  YLMSWPFQDVLCRKIVISIDYYNMFSTIFTLTMSVDRYIAVCHPVKALDERTPLKAKII 178
        nvcnwilssaiglpvmfmatlkyrg-s-idetltfshtpw-ywenlkicviglifafimp 244
Db       188  nvcnwilssaiglpvmfmatlkyrg-s-idetltfshtpw-ywenlkicviglifafimp 244
        |:|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY       179  NICIWLIASSVGISAIVLGTKVRPDYDIIECSIQPDDDEYSWMDLFMKICVFVAFAVIP 238
        vlitvcyglmrlrksvrmlsgskekdrrlrirtmvlvvvavfiwcwtphiyvlka 304
Db       245  vlitvcyglmrlrksvrmlsgskekdrrlrirtmvlvvvavfiwcwtphiyvlka 304
        ||||| ||| |||||||||::|||::|||::|||::|||::|||::|||::|||::|||
QY       239  VLIITVCYTMLRLRKSVALLSGSREDNRLLRIITKLVLVVAVFIICWTPIHIFILVEA 298
        litipettfgtvswhfcialgytnsclnpvylyafldenikrcrfeciptsstieqgst 364
Db       305  litipettfgtvswhfcialgytnsclnpvylyafldenikrcrfeciptsstieqgst 364
        |:::||| | ||||||||| ||||||||| ||||||||| ||||||||| |||::|
QY       299  LGSTSHSTAALSSSYFCIALGTINSSLNPVLYAFLDENFKRCRFECFPICKRMERQSTN 358
        rrvqrntrehpstantv 380
Db       365  rrvqrntrehpstantv 380
        ||| |||::|||::|||
QY       359  RVR-NTVQDPASMRDY 373

RESULT      13
ENTRY       I38657             #type complete
TITLE       delta opiate receptor - human
ORGANISM    Homo sapiens #common_name man
DATE         06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS  I38657
REFERENCE    Simonin, F.; Befort, K.; Gaveriaux-Ruff, C.; Matthes, H.;
              Nappey, V.; Lannes, B.; Micheleletti, G.; Kliefer, B.
              Mol. Pharmacol. (1994) 46:1015-1021
              The human delta-opioid receptor: genomic organization, cDNA
              cloning, functional expression, and distribution in human
              brain.
#authors     Simonin, F.; Befort, K.; Gaveriaux-Ruff, C.; Matthes, H.;
              Nappey, V.; Lannes, B.; Micheleletti, G.; Kliefer, B.
#journal     Mol. Pharmacol. (1994) 46:1015-1021
#title       The human delta-opioid receptor: genomic organization, cDNA
              cloning, functional expression, and distribution in human
              brain.
#cross-references MCTD:95107267
#accession   I38657
#status      preliminary; translated from GB/EMBL/DDBJ
#molecule_type mRNA
#residues    1-372  ##label RES
#cross-references EMBL:U10504; NID:g501144; CDS_PID:g501145
SUMMARY      #length 372  #molecular-weight 40368  #checksum 1688

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Best Local Similarity      63.1%; Pred. No. 2.14e-233;
Matches     217; Conservative   60; Mismatches    58; Indels     9; Gaps     8;

Db       15  lfanasdypsa-a-cpsaganasgppgarsas-slalaaitalsaycavglignvlwm 71
        |::||| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
QY       22  LLPNSSSWEPNWMAESDSNGSVGEDQLSAHISPAPVITTAVSVVFVGVGLGNSLVM 81
        llmpnswwepnwmaesdsngsvgedqlsaahispapvittavsvvfvgvlgvnslvm 81
Db       72  fgivirytkmtatniyifnlaladalstlpfgsakylmetwpfgellckavlsideyn 131
        |:|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY       82  FVIIRYTKMTAINTIYNFLALADALTTPFQSAVYIMNSWPFGDVLCRVISIDYYN 141
        fgivirytkmtatniyifnlaladalstlpfgsakylmetwpfgellckavlsideyn 131
        |:|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       132  mftsifcltmssvdryiaavchpvkaldftrpakakliniciwlasygvvpimymavtrp 191
        ||||||| cltmssvdryiaavchpvkaldftrpakakliniciwlasygvvpimymavtrp 191
QY       142  MFTSIPTLTMSVDRYIAVCHPVKALDERTPLKAKIINICIWLASSVGISAIVLGGTKV 201
        ||||||| tsiptltmssvdryiaavchpvkaldfertplkakiiNICIWLAASSVGISAIVLGGTKV 201
Db       192  rdga-vv-cmlqfsp--swywdvckicvflfafvwpiilitvcyglmllrlsrvis 247
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QY	202	REDVDVIECSLQFPDDEXSW-WDLFMKICVFVFAFVPIVLIITIVCYTLMILRLKSVRLIS	260
Db	248	gskekdrslrritmvlvvvgafvvcwaphifvlywtlvdidrrdplvvaalhcialg	307
QY	261	GSREKDRNLRRITKLVLVVAVFIICWTPHIFLVEALGSTSHSTA-ALSSYFCIALG	319
Db	308	yansslnpvlyafldenfkrcfrqlcrkpcgrdpssfsararea	351
QY	320	YTNSSLNPVLYAFLDENFKRCFRDPCFPKMRMERGSTNRVRNT	363
RESULT	14	S34592	#type complete
ENTRY			delta opioid receptor - rat
TITLE			#formal_name Rattus norvegicus #common_name Norway rat
ORGANISM			10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change
DATE			06-Sep-1996
ACCESSIONS			S34592; S34592
REFERENCE			S34592
#authors			Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.
#journal			FEBS Lett. (1993) 327:311-314
#title			Primary structures and expression from cDNAs of rat opioid receptor delta- and mu-subtypes.
#accession			S34592
##molecule_type	mRNA		
##residues	1-372	#label	FUK
REFERENCE			I56571
#authors			Aboud, M.E.
#journal			J. Neurosci. Res. (1994) 27:714-719
#title			Molecular cloning and expression of a rat delta opioid receptor from rat brain.
#accession			I56571
##status			Preliminary; translated from GB/EMBL/DDBJ
##molecule_type	mRNA		
##residues	1-372	#label	RES
##cross-references			EMBL:U00475; NID:g403488; CDS_PID:g514211
GENETICS			
#gene		dor1	
SUMMARY		#length 372	#molecular-weight 40449 #checksum 2221
Query Match		56.7%;	Score 1610; DB 14; Length 372;
Best Local Similarity		65.6%;	Pred. No. 4.55e-233;
Matches	214;	Conservative	55; Mismatches 48; Indels 9; Gaps 7;
Db	15	llanvsdtfpsafpsasanasgspgar--sas-slalalatalysavcavglgnvlym	71
QY	22	LLPNSSSWEPNWAESDSNGSVSEDOQLESAAHISPAIPVITAVYSVFVVGVLGNSLWM	81
Db	72	fgivrytklktatniyifnlaladalatatstlpfgsakylmetwpgellckavlsidynn	131
QY	82	FVIRYTKMKRATNIYIFNLALADALVTTMPFGSAVYIMNSWPEGDVLCKIVISIDYNN	141
Db	132	mftsiftltmmsvdryiaavchpvykaldfrtpakakliniciwiiasvgvvpimvamtqp	191
QY	142	MFTSIFTLTMSVDRYIAVCHPVKALDERTPLKAKIINICIMWLLASSVGISAIVLGITKV	201
Db	192	rdga-vv-ctlgfpp--swywdvtvkicvflfafvvpillitvcyglmllrlrsvrlis	247
QY	202	REDVDVIECSLQFPDDEXSW-WDLFMKICVFVFAFVPIVLIITIVCYTLMILRLKSVRLIS	260
Db	248	gskekdrslrritmvlvvvgafvvcwaphifvlywtlvdidrrdplvvaalhcialg	307
QY	261	GSREKDRNLRRITKLVLVVAVFIICWTPHIFLVEALGSTSHSTA-ALSSYFCIALG	319
Db	308	yansslnpvlyafldenfkrcfrqlc	333
QY	320	YTNSSLNPVLYAFLDENFKRCFRDPC	345
RESULT	15	B48227	#type complete
ENTRY			delta opioid receptor 1 - mouse
TITLE			

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ORGANISM      #formal_name Mus musculus #common_name house mouse
DATE          26-May-1994 #sequence_revision 26-May-1994 #text_change
              01-Dec-1995
ACCESSIONS    B48227; S37807; A48685
REFERENCE     A48227
#authors      Yasuda, K.; Raynor, K.; Kong, H.; Breder, C.D.; Takeda, J.;
              Reisine, T.; Bell, G.I.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1993) 90:6736-6740
#title        Cloning and functional comparison of kappa and delta opioid
              receptors from mouse brain.
#accession    B48227
#status       preliminary
#molecule_type mRNA
#residues     1-372 #label YAS
#cross-references GB:L11064
REFERENCE     S37807
#authors      Kleffer, B.L.; Befort, K.; Gaveriaux-Ruff, C.; Hirth, C.G.
#submission   Submitted to the EMBL Data Library, February 1993
#accession    S37807
#status       preliminary
#molecule_type mRNA
#residues     1-372 #label KIE
#cross-references EMBL:L06322
REFERENCE     A48685
#authors      Bzdega, T.; Chin, H.; Kim, H.; Jung, H.H.; Kozak, C.A.; Klee,
              W.A.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9305-9309
#title        Regional expression and chromosomal localization of the delta
              opiate receptor gene.
#cross-references MJD:94022364
#accession    A48685
#status       preliminary
#molecule_type mRNA
#residues     8-372 #label BZD
#cross-references NCBI:138618; NCBI:138619
#experimental_source NC108-15 hybrid cells
#note          sequence extracted from NCBI backbone
KEYWORDS       brain; G protein-coupled receptor; glycoprotein;
              phosphoprotein; transmembrane protein
SUMMARY        #length 372 #molecular-weight 40561 #checksum 3372

Query Match      56.38; Score 1597; DB 14; Length 372;
Best Local Similarity 66.78; Pred. No. 6,11e-231;
Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5;

Db 47 alaiaitalysavcavglgnvfmfgivrytklktatniyifnladalatstlpfqs 106
QY 57 AIPVITAVYSVVFVVGGLVGNLMEVFIIRYTKMKLTATNIYIFNLALADALVTTMPFQS 116

Db 107 akylmetwpgfjellckavlsidyymftsifltmmsvdryiaavchpvcakldfrtpakak 166
QY 117 AVYLMNSWPFQDYLCKIVISIDYXNMTSIFLTMTMSVDRYIAVCHPVKALDFRTPAKAK 176

Db 167 llnictlwlavsgvypimvmavtqprdga-vv-cmlqfpp--swywdvtvklcvflfa 222
QY 177 IINICIWLLASSVGSISAIIVLGGTKVREDVDVIECSLQFPDEXSW-WDLFMKICVFVFAF 235

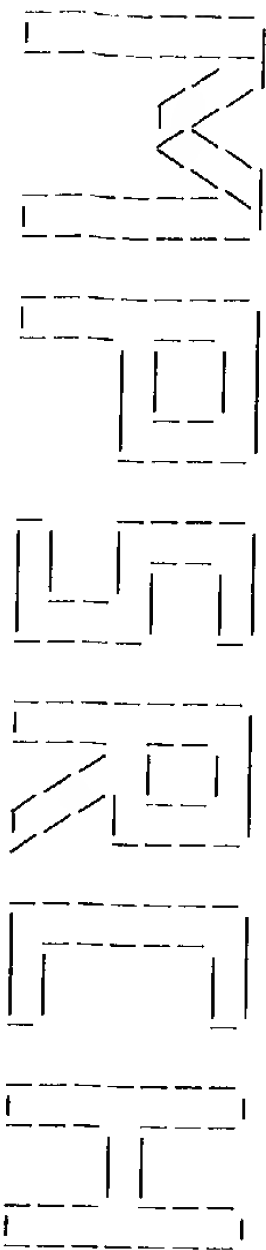
Db 223 vvpililtvcyglmllrlsrvlsgskekdslrritrmvlyvvgaafvvcwapihifvi 282
QY 236 VIPVLIIIVCYTLMILRLKSVRLSGSREKDRNLRRITKLVVYAVFIICWTPIHIFIL 295

Db 283 vwtlydlnrrdplvvaalhclalyansslnpvlyafldenfkrcfrqlcrtpcgrqep 342
QY 296 VEALGSTSHSTA-ALSSYFICIALGYTNSINPVLVYAFLDENFKRCFRDPCPIKRMER 354

Db 343 gslrrprga 351
QY 355 QSTNRVRNT 363
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Search completed: Tue Aug 26 14:52:07 1997  
Job time : 104 secs.





(TM)

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Msrch\_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Aug 26 08:46:08 1997; MasPar time 173.41 Seconds

Tabular output not generated. 800.037 Million cell updates/sec

Title: >US-08-292-694A-1  
Description: (1-1410) from US08292694A.seq  
Perfect Score: 1410  
N.A. Sequence: 1 GCGCACCCTTGCATGCCCAA.....AACCCAGATTACACTGCAG 1410  
Comp: CGCGTGGACGACTAGGGTT.....TTGGGTCTAATGTTCACGTC

Scoring table: TABLE default  
Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 134151 seqs, 49196315 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-genesq27  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 9.371; Variance 5.282; scale 1.774

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1410	100.0	1410	13	Q75926	Mouse kappa opioid re 0.00e+00
2	1129	80.1	2481	15	Q86725	Mammalian kappa opioi 0.00e+00
3	838	59.4	1142	20	T12550	Human kappa opioid re 0.00e+00
4	668	47.4	1000	13	Q75931	Human kappa opioid re 0.00e+00
5	311	22.1	2070	12	Q79199	Rat mu-subtype opioid 6.23e-205
6	309	21.9	1618	14	Q89222	Rat mu opioid recepto 1.96e-203
7	309	21.9	1618	14	Q89223	Transcription regulat 1.96e-203
8	309	21.9	1821	10	Q56705	Partial sequence of t 1.96e-203
9	291	20.6	2272	13	Q75927	Sequence of murine de 5.67e-190
10	291	20.6	2272	13	Q75927	Mouse delta opioid re 5.67e-190
11	289	20.5	1610	14	Q89226	Human mu opioid recep 1.77e-188
12	289	20.5	2160	15	Q93102	Human mu opiate recep 1.77e-188
13	276	19.6	2216	11	Q66656	Murine delta opioid r 8.97e-179
14	230	16.3	829	10	Q56703	Partial sequence of t 1.45e-144
15	220	15.5	1567	14	Q89233	Rat opioid receptor c 3.67e-137
16	218	15.5	1330	13	Q75928	Mouse opioid receptor 1.11e-135

17	218	15.5	2706	15	Q92972	Rat opiorph receptor 1.11e-135
18	207	14.7	2600	14	Q90096	Mouse kappa-3 opioid 1.47e-127
19	195	13.8	2447	10	Q56702	Partial sequence of t 1.02e-118
20	97	6.9	1265	7	Q45654	Murine somatostatin r 6.32e-48
21	91	6.5	1047	2	Q10572	Human Natriuretic Pep 9.84e-44
22	78	5.5	1047	2	Q10572	Human Natriuretic Pep 9.35e-35
23	77	5.5	1518	14	Q83682	Epsilon opioid recept 4.51e-34
24	78	5.5	1634	7	Q45653	Human somatostatin re 9.35e-35
25	75	5.3	1110	5	Q29155	Pituitary somatostati 1.04e-32
26	73	5.2	1244	7	Q45656	Murine somatostatin r 2.38e-31
27	67	4.8	822	5	Q29156	Brain somatostatin re 2.65e-27
28	68	4.8	1130	23	T09250	Human somatostatin re 5.66e-28
29	67	4.8	1296	7	Q45657	Human somatostatin re 2.65e-27
30	68	4.8	1351	7	Q45655	Human somatostatin re 5.66e-28
31	68	4.8	1796	7	Q45658	Murine somatostatin r 5.66e-28
32	56	4.0	1054	14	Q83681	Epsilon opioid recept 4.95e-20
33	46	3.3	1162	11	Q66170	Seven transmembrane r 1.21e-13
34	46	3.3	2254	11	Q66167	Seven transmembrane r 1.21e-13
35	45	3.2	1200	16	Q95036	Rat hippocampal neuro 5.08e-13
36	45	3.2	1556	16	Q95035	Rat hippocampal neuro 5.08e-13
37	44	3.1	1495	11	Q62695	C-C chemokine recepto 2.12e-12
38	41	2.9	91	9	Q51746	Oligonucleotide probe 1.47e-10
39	39	2.8	91	9	Q51746	Oligonucleotide probe 2.36e-09
40	40	2.8	204	1	N81164	Base substituted E.co 5.91e-10
41	40	2.8	204	1	N81164	Base substituted E.co 5.91e-10
42	39	2.8	1900	11	Q66162	Partial coding sequen 2.36e-09
43	39	2.8	2058	11	Q66153	Putative seven transm 2.36e-09
44	39	2.8	2154	11	Q64125	Epstein Barr virus in 2.36e-09
45	39	2.8	2160	11	Q66160	Putative seven transm 2.36e-09

ALIGNMENTS

RESULT 1  
ID Q75926 standard; DNA; 1410 BP.  
AC Q75926:  
DE Mouse kappa opioid receptor MOR1 cDNA.  
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;  
KW transmembrane domain; somatostatin; receptor; human; expression vector;  
KW truncate; chimaeric; assay; probe; ss.  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT CDS 186..1328  
FT /\*tag= a  
FT /product= mouse kappa opioid receptor  
FT PN W09428132-A.  
PD 08-DEC-1994.  
PE 20-MAY-1994; U05747.  
PR 20-MAY-1993; US-066296.  
PR 30-JUL-1993; US-100694.  
PR 05-NOV-1993; US-147592.  
PA (ARCH-) ARCH DEV CORP.  
PI Bell GI, Reisine T, Yasuda K;  
DR WPI; 95-022804/03.  
DR P-PSDB; R67669.  
PT Polynucleotides and peptides derived from opioid receptor  
PT polypeptides - for use in therapeutic compositions and in  
PT screening assays for useful drug substances.  
PS Claim 10; Page 207-211; 300pp; English.  
CC The nucleotide sequence of the novel mouse kappa opioid receptor gene  
CC MOR1. The gene was isolated from a mouse brain cDNA library using a  
CC fragment (amplified from the cDNA library with primers Q75929-30) as a  
CC probe. The primers are based on the conserved sequences present in the  
CC second and third transmembrane domains of somatostatin (SRIF) receptor  
CC subtypes SSTR1, SSTR2 and SSTR3. The 1.2 kb PstI fragment from the mouse  
CC kappa opioid receptor clone, lambda msl-1, was subcloned into the CMV  
CC promoter-based expression vector pCMV-6b. The resultant construct  
CC pCMV-msl-1 was transfected into COS-1 cells for protein production. The  
CC gene encoding the opioid receptor can be used to produce complete,  
CC truncated or chimaeric opioid receptor proteins. The opioid receptors  
CC thus produced are useful for the development of novel assays designed to  
CC select or improve substances, capable of interacting with the opioid



QY 170 AGCTGACGCGCTCACCATGAGTCCCCCATTCAGATCTCCGAGGAGATCCAGGCCCTAC 229

Db 155 ctgtgtctccagtgcttgccctactcccccaacagcagctcttggttccccaaactggygcga 214

QY 230 CTGCTCTCCAGTGTCTTGCCCTCTCCCCACAGCAGCTCTTGTTCCCAACTGGGCAGA 289

Db 215 atcggacagcaatgycagtttgggtccaggagcagcagctgagcccgcgacatctc 274

QY 290 ATCCGACAGTAATGGCAGTGTGGGCTCAGAGGATCAGCAGCTGGAATCCGCCACATCTC 349

Db 275 tccagccatccctgttlatcatcacccgtgtctactctgtgtgtgttgggtggttagt 334

QY 350 TCCGGCCATCCCTGTATCATCACCGCTGTCTACTCTGTGGTATTTGTGTGGCTTAGT 409

Db 335 gggcaattccctggtcatgtttgtcatcatccgatatacaaagaatgaagaccgcaacca 394

QY 410 GGGCAATTCTCTGTGTCATGTTGTATCATCCGATACACGAAGATGAAGACCGCAACCA 469

Db 395 catcatatatttaacctgtgttggtggcagatgcttggttactaccactatggccctcca 454

QY 470 CATCTACATATTTAACCTGGCTTTGGCAGATGCTTTGGTTACTACCACTATGCCCTTCA 529

Db 455 gagtgtgtctacttgatgaattcttggcccttggagagatgtctgtgaagatgtcat 514

QY 530 GAGTGTCTACTTGTATGAATTTCTTGCCCTTTGGAGATGTCTATGCAAGATGTGCAT 589

Db 515 ttccattgactactacaacatgttltacaagcatattcaacctgacatgatgagtgtga 574

QY 590 TTCCATTGACTACTACACATGTTTACCAGCATATTCACCTTGACCATGATGAGTGTGA 649

Db 575 ccgctacattgcccgtgtgcccaccctgtgaagcttggatttccgaacaccttgaagc 634

QY 650 CCGCTACATTGCTGTGTGCCACCCCTGTGAAGCTTTGGACTTCCGAACACCTTTGAAAGC 709

Db 635 aaagatcatcaacatctgcatgttgctactggtcatcatctgttggatatacgcgatagt 694

QY 710 AAAGATCATCAACATCTGCATTTGGCTCCTGGCATCATCTGTTGTAATACGCGATAGT 769

Db 695 ccttgagggacccaagtcaaggagagatgtgatgtcatltyaatgctccttgcaagttcc 754

QY 770 CCTTGAGGCACCAAGTCAAGGGAAGATGTGATGTCAITGAATGCTCCTTGACAGTTTCC 829

Db 755 tgatgatgaatatctcctggtgtyggacctcttcataagaatctgtgtcttgccttgcct 814

QY 830 TGATGATGAATAATCTCTGTGGGATCTCTTCATGAAGATCTGTGTCTTCGCTTTGCCCT 889

Db 815 tgtlatccctgtcttaatcatcatatgtgtctgtacaacctgatgatccctgcgcttgaag 874

QY 890 TGTGATCCCAAGTCTCATCATCATGTGTGTGTACACCCCTGATGATCCTGCGCCTGAAGAG 949

Db 875 tgtccggctcctctcctcgggtctcgcgagagaaggaaccgaaatctccgcgcgataccaagct 934

QY 950 TGTCCGGCTCCTGTCTGTGGCTCCCGAGAGAGAGACCGAAATCTCCGCCGATCACCAAGCT 1009

Db 935 ggtgctgtagtggttgcagctcttcataatctgttggaccccccatccacatcttatcct 994

QY 1010 GGTGCTGCTAGTAGTTCGAGTCTTCATCATCTGTTGGACCCCCATTCACATCTTATCCT 1069

Db 995 ggtcgaagctctaggcaagcaacctctcaacagcaacagctgtctctctctagctattactctg 1054

QY 1070 GGTGGAAGCTCTGGGAAGCACCTCCACAGCACAGCTGCCCTCTCCAGCTATTATTCTG 1129

Db 1055 cattgccttgggttatataccaacagcagcttgaatccctgttctctatagccttcttgatca 1114

QY 1130 TATGCTCTTGGGTATATCCACACAGCAGCCTGAATCCTGTCTCTATGCTTCTTGATGA 1189

Db 1115 aaactcaagcgtgttlttaggacttctgcttccccattaaagatgcgaatgagcgcca 1174

QY 1190 AAAGTTCAAGCGGTGTTTAGGSACTTCTGCTTCCCTATTAAAGATGCGAATGGAGCGCA 1249

Db 1175 gagcaacaacagagtttagaacaacagttcaggatcctgcttccatgagagatgtgtgtgg 1234

QY 1250 GAGCACCAATAGAGTTAGAACAACAGTTCAGGATCCTGCTTCCATGAGAGATGTGGGAGG 1309

Db 1235 gatgaataagccagtatgtactagtcatggaatgtcttccctattgttctcgggtagaga 1294

QY 1310 GATGAATAGCCAGTATGACTAGTGTGGAATGTCTTCTTAATGTCTCCAGGTAGAGA 1369

Db 1295 agagttcaatgatcttggtttaacccagattaccactgcag 1335

QY 1370 AGAGTCAATGATCTTGTTTAACCCAGATTACAACCTGCAG 1410

RESULT 3

ID T12550 standard; cDNA; 1142 BP.

AC T12550;

DT 03-SEP-1996 (first entry)

DE Human kappa opioid receptor cDNA.

KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular; neurology; diagnosis; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..1142

FT /product= kappa\_opioid\_receptor

FT /note= "incomplete termination codon"

PN WO9601898-A1.

PD 25-JAN-1996.

PF 07-JUL-1995; F00912.

PR 11-JUL-1994; FR-008531.

PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.

PI Kieffer B, Simonin F;

DR WPI; 96-097628/10.

DR P-PSDB; R88722.

PT New nucleic acid encoding the human Kappa opioid receptor - useful in diagnosis and therapy, and for isolating receptor ligands and PT modulators

PS Claim 3; Page 13-15; 30pp; French.

CC This sequence codes for the human kappa opioid receptor and was CC obtained from two overlapping cDNA fragments isolated from a CC human placental cDNA library. The fragments were amplified from CC the library using PCR primers based on the sequence of human CC genomic clones which hybridised with a murine delta receptor cDNA CC probe. Nucleotide probes derived from the kappa opioid receptor CC coding sequence are useful for diagnosis of neurological, cardio- CC vascular and psychiatric disorders associated with opioid CC receptors.

SEQ Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T;

Query Match 59.4%; Score 838; DB 20; Length 1142;

Best Local Similarity 86.7%; Pred. No. 0.00e+00;

Matches 990; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

Db 1 atggaactccccgatccagatcttccgggggagccgggacctactgccccgagcgcc 60

QY 186 ATGGAAGTCCCCCATTCAGATCTTCGAGAGAGATCCAGGCCCTAACCTGCTCTCCAGTGTCT 245

Db 61 tgcctgccccccaacagcagcgctgttcccggtctgggcgcgagcccgacagcaagcgc 120

QY 246 TGCTTCTCCCAACAGCAGCCTGTGGTTCCCAACTGGGCGAATCCGACAGTAATGGC 305

Db 121 agcgccggtcgcgagagcgcgagctgagcccgcgacacatctcccgccatcccggtc 180

QY 306 AGTGTGGGCTCAGAGGATCAGCAGCTGGAGTCCGGCGACATCTCTCCGGCCATCCTGTGTT 365

Db 181 atcaacaagcggtctactccgtagtgttcgtcgtgggtgtgtggcaactgcgtgtc 240

QY 366 ATCATCACCGCTGTCTACTCTGTGTGTAATTTGTGTGGGCTTAGTGGAATTCCTGTGCTC 425

Db 241 atgttcgtgatcatccgatacaacaagaatgaagagacagcaaccaattacatttaac 300

QY 426 ATGTTTGCATCATCCGATACAGAACGAAGATGAAGACCGCAACACATCTACATATTTAAC 485

Db 301 ctggccttggcagatgctttagttactacaacacatgcccttcagagtaagctacttg 360

QY 486 CTGGCTTTGGCAGATGCTTGGTTACTACCACTATGCCCTTTCAGAGATGCTGCTACTTG 545



Db	361	atgaattccctgagcccttbtggsgaatgtgctgtlgoaagatagtaatttccattgattactac	420
QY	546	ATGAATTCCTGGCCCTTTGGAGATGTGCTATGCAAGATTGTCAATTTCCATTGACTACTAC	605
Db	421	aacatgttcaccagcatcttcaaccttgaaaccaatgatgagcgttgaccgctacattgcccgtg	480
QY	606	AACATGTTTACCAGCATATTCACCTTGACCATGATGAGTGTGGACCGCTACATTGCTGTG	665
Db	481	tgccaccccgtgaagyccttggacttcgcacacaccccttgaagycaaagatcatcaatac	540
QY	666	TGCCACCCCTGTGAAGCTTTGGACCTCCGAAACACCTTTGAAAGCAAGATCATCAACATC	725
Db	541	tgcatctgctgctgtgtcgtcatctgtttggcatctctgcaatagtccttggagycaccaaa	600
QY	726	TGCATTTGGCTCCTGGCATCATCTGTTGGTAATACAGCGATAGTCCTTGAGAGCACCAAA	785
Db	601	gtcaggggaagacgctgcgatgtcatattgagtgctctccttgcaagtlcccaagatgactacc	660
QY	786	GTCAGGGAAGATGTGGATGTCAATTGAATGCTCCTTGCAAGTTCCGTGATGATGAATATTC	845
Db	661	tggtgggaacctcttcatlgaagatctgcgtcttcatcttttgcccttgatgccctgtccctc	720
QY	846	TGTTGGGATCTCTTCATGAAGATCTGTGTCTTTCGTCTTTGCCCTTGTGATCCCAAGTCCTC	905
Db	721	atcatcatcgtctctgtacacacctgatgatcctgcgtctcgaagagcgtccgctcccttct	780
QY	906	ATCATCATTTGCTGTCTACACCCCTGATGATCCTGGCCCTGAAGAGTGTCCGGCTCCTGTCT	965
Db	781	ggctcccgagagaagaatgcgaacctgcgtagatgataccagaactgctcctgtgtgtgtg	840
QY	966	GGCTCCCGAGAGAAGAACCGAAATCTCCGCCGATCACCAAGCTGTGTGTGTAGTAGTT	1025
Db	841	gcagctcttcgtcgtctgtgagctcccatcaacatatcaaccctggtlgsaggtctggsg	900
QY	1026	GCAGTCTTCATCATCTGTTGGAACCCCATTCACATCTTTATCCCTGGTGGAGGCTCTGGGA	1085
Db	901	agcacctcccacagcaacagctgctctctccagctattactctcgtcagccttaggctat	960
QY	1086	AGCACCTCCACAGCACAGCTGCCCTCTCCAGCTATTATTCTGTATTTGCCCTGGGTTAT	1145
Db	961	accacagtagcctgaatcccatctctctacggccttcttgatgaaaaacttcaagcgygtg	1020
QY	1146	ACCAACAGCAGCCCTGAATCCTGTTCTCTATGCCCTTTCTGGATGAACCTTCAAGCGGTGT	1205
Db	1021	ttccgggactctgtcttccactgaagatgagagtgagagcggcagagcactagcagatc	1080
QY	1206	TTTAGGACTTCTGCTTCCCTATTAAAGATGCGAATGGAGCGCCAGAGCAACCAATAGAGTT	1265
Db	1081	cgaatacacgttccagatccctgttaacctgagggacatcgatgagatgaataaaccagta	1140
QY	1266	AGAAACACAGTTCAAGATCCTGCTTCCATGAGAGATGTGGAGGGGATGAATTAAGCCAGTA	1325
Db	1141	tg 1142	
QY	1326	TG 1327	

RESULT	4	
ID	Q75931	standard; DNA; 1000 BP.
AC	Q75931;	
DT	18-AUG-1995	(first entry)
DE	Human kappa opioid receptor partial cDNA fragment.	
KW	Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;	
KW	transmembrane domain; somatostatin; receptor; human; expression vector;	
KW	truncate; chimaeiric; assay; probe; ss.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	CDS	102..989
FT	/*tag= a	
FT	/product= partial human kappa opioid receptor	
PN	W09428132-A.	
PD	08-DEC-1994.	

PF 20-MAY-1994; U05747.  
PR 20-MAY-1993; US-066296.  
PR 30-JUL-1993; US-100694.  
PR 05-NOV-1993; US-147592.  
PA (ARCH-) ARCH DEV CORP.  
PI Bell GI, Reisine T, Yasuda K;  
DR WPI: 95-022804/03.  
P-PSDB; R67672.  
PT Polynucleotides and peptides derived from opioid receptor  
PT polypeptides - for use in therapeutic compositions and in  
PT screening assays for useful drug substances.  
PS Claim 10; Page 236-239; 300pp; English.  
CC The partial nucleotide sequence of the novel human kappa receptor  
CC gene. The gene was isolated from a human brain hippocampus cDNA library  
CC using a probe from the mouse kappa opioid receptor gene (Q75926). The  
CC gene is missing the N-terminal sequence. The C-terminal sequence is  
CC very similar to the mouse kappa opioid receptor sequence. Of the  
CC C-terminal 293 amino acids, 281 residues are identical and 6 residues  
CC have conservative substitutions. The gene encoding the human opioid  
CC receptor can be placed in a suitable expression vector for production of  
CC the protein in a cell. The opioid receptors thus produced are useful for  
CC the development of novel assays designed to select or improve substances,  
CC capable of interacting with the opioid receptor proteins, for use in  
CC diagnosis, drug design and therapeutic applications.  
SQ Sequence 1000 BP; 238 A; 253 C; 225 G; 278 T;

Query Match	47.4%;	Score 668;	DB 13;	Length 1000;
Best Local Similarity	87.6%;	Pred. No. 0.00e+00;		
Matches	789;	Conservative	0;	Mismatches 109;
			Indels	3;
			Gaps	2;

D	b	100	gatacaacaagaatgaagacagcaaccaacattacatatattaacctggtcttggcagatg	159
Q	Y	442	GATACACGAGATGAAGACCGCAACCAACAATCTACATATTTAAACCTGGCTTGGCAGATG	501
D	b	160	ctttaagtactacaacacatgcccctttcagagtagcgtctactgtatgaattccctggcctt	219
Q	Y	502	CTTTGGTTACTAACCACTATGCCCTTTCAGAGTGGCTGTCTACTGTATGAATTTCTGGCCTT	561
D	b	220	ttggggatgtgctgtgcaagatatagtaatttccattgtattactacaacatggttcaaccagca	279
Q	Y	562	TTGGAGATGTGCTATGCAAGATTGTCAATTTCCATTGACTACTACAACATGTTTACCAACA	621
D	b	280	tcttcacaccttgacaacatgatagcgttggaccgctacattgcccgtgtgccaccccgtyaag	339
Q	Y	622	TATTCACCTTGACCATGATGAGTGTGGACCGCTACATTTGCTGTGTGCCACCCCTGTGAAG	681
D	b	340	ctttgacctccgcacacaccccttgaagycgaagaatcacataatctgcactgctgctgt	399
Q	Y	682	CTTTGGACTTCGGAACAACCTTTGAAGCAAGATCATACATCTGCATTTGGCTCCTGG	741
D	b	400	cgtcatctgttggcgcactctcgaatagtccttggagycaccaaaagtcaagggaaagtgtcg	459
Q	Y	742	CATCATCTGTGTGGTATATACAGCGATAGTCTCTTGAGGCAACCAAGTCAGGGAAGATGTGG	801
D	b	460	atgtcatctgaatgctgctgtcagttccocagatgatgactactcctggttgggacctcttca	519
Q	Y	802	ATGTCATTGAATGCTCCTTGCAAGTTTCCGTGATGATGAATATTCCTGGTGGGATCTTTCA	861
D	b	520	tgaagatctgcgctcttcacatcttttgccttcgtcatccctgctcctcatcatcatcgtctgct	579
Q	Y	862	TGAAGATCTGTGTTCTTTCGTTTTCCTTTGTCCTTGTGATCCCAAGTCCATCATCATTTGTCTGCT	921
D	b	580	acaccctgatgatccctgcgtctcgaaganngtccggctcccttcttctggtctcccgagayaag	639
Q	Y	922	ACACCCCTGATGATCCTGCGCCTGGAAGAGTGTCCGGCTCCTGTGTGGCTCCCGAGAGAAGG	981
D	b	640	atnncaacctgcgtagatcaccaagactgltcctggtgtgtgtgagcaagtcttcgtcgtct	699
Q	Y	982	ACCGAAATCTCCGCCGCATCACCAAGCTGTGTGCTGTAGTAGTTGCAATCTTCATCATCT	1041
D	b	700	gctggaactcccatlccacatatattcactcctgtgtggaggtcctgtgggagcacctccacagca	759
Q	Y	1042	GTTGGACCCCCCATTCACATCTTTATCTTGTTGAGGCTCTGGGAAGCACCTCCCAACAGCA	1101



Db 760 cagctgctctccagctattacttctgcatcgcccttagctataccaacagtagcctga 819  
QY 1102 CAGCTGCCCTCTCCAGCTATTATTCTGTATGTGCTTGGGTTATACCAACAGCAGCCTGA 1161  
Db 820 atccattctctacgcttcttctgtatgaaacttcaacggtgttccgagacttctgt 879  
QY 1162 ATCCTGTCTCTATGCTTCTGTGATGAAACTTCAAGCGGCTTTTAGGGACTTCTGCT 1221  
Db 880 ttccactgaagatgagnatggagcgcnagagcactagcagagtcgcgaataacagttcag 939  
QY 1222 TCCCTATTAAAGATGCCAATGGAGCGCCAGAGCACCAATAGAGTTAGAAACACAGTTCCAG 1281  
Db 940 atcctgcttacctggagagatcgatggatgataaataaaccagtatgactagtcgtg 999  
QY 1282 ATCCTGCTTCCATGAG--AGAT-GTGGAGGAGATGAATAAGCCAGTATGACTAGTCGTGG 1338  
Db 1000 a 1000  
QY 1339 A 1339

RESULT 5  
ID 079199 standard; cDNA; 2070 BP.  
AC 079199;  
DI 19-APR-1995 (first entry)  
DE Rat mu-subtype opioid receptor cDNA.  
KW Mu-subtype opioid receptor; MSOR; drug addiction; ds.  
OS Rattus rattus.  
FH Key Location/Qualifiers  
FT CDS 83..1154  
FT /product= Mu-subtype\_opioid\_receptor  
PN EP-612845-A.  
PD 31-AUG-1994.  
PF 09-FEB-1994; 101968.  
PR 26-FEB-1993; US-026140.  
PA (AMCY ) AMERICAN CYANAMID CO.  
PI Corbett MJ, Eppler CM, Shieh H, Zysk JR;  
DR WPI; 94-265963/33.  
DR P-PSDB; R65188.  
PT Pure mu-type opioid receptor protein - and nucleic acid coding  
PI for it  
PS Claim 1; Fig 11; 39pp; English.  
CC R65188 is the rat mu-subtype opioid receptor protein purified  
CC from rat brain membranes, with biotinyl-b-endorphin (R56666)  
CC as its ligand. It is encoded by the nucleotide sequence 079199  
CC which was synthesised using 071022 and 071023 as PCR primers.  
CC R65188 is useful for identifying other receptor subtypes, for  
CC screening new opioid ligands, and for studying mechanisms of  
CC opioid action, e.g. drug addiction.  
SQ Sequence 2070 BP; 526 A; 564 C; 423 G; 557 T;

Query Match 22.1%; Score 311; DB 12; Length 2070;  
Best Local Similarity 70.6%; Pred. No. 6.23e-205;  
Matches 609; Conservative 0; Mismatches 244; Indels 9; Gaps 8;

Db 171 ttaccatcatggccctactctatctgtctgtgtagtgccctcttcggaacttcctg 230  
QY 364 TTATCATCACCGCTGTCTACTCTGTGTTATTGTGGGCTTAGTGGCAATTCTCTGG 423  
Db 231 tcatgtatgtgattgtaataacacaaatgaagactgccaacaacatctacatttca 290  
QY 424 TCATGTTTGTATCATCCGATACACGAAGATGAAGACCGCAACCAACATCTACATTTA 483  
Db 291 acctgctctgacagacgcttagcagacagtagacagccttcagagtgtaactacc 350  
QY 484 ACCTGGCTTTGGCAGATGCTTTGGTTACTACCACTATGCCCTTTCAGAGTGTCTACT 543  
Db 351 tgatggagacatggccttcggaacacatcctctcgaagatcgtgatcctaagattact 410  
QY 544 TGATGAATTCCTGGCCTTTTGGAGATGTGCTATGCAAGATTTGTCATTTCATTGACTACT 603

Db 411 acaacatgttcaaccagatatccacctctgcaccatgagcgtgagccgtacattgctg 470  
QY 604 ACAACATGTTTACACAGCATATTCCACTTGACCCATGATGAGTGTGGACCCGCTACATTGCTG 663  
Db 471 tctgccaccagtcacaagccctgatttccgtaacccccgaataatgccaaatcgtcaag 530  
QY 664 TGTGCCACCCCTGTGAAGCTTTGGACTTCCGACACCTTTGAAAGCAAGATCATCAACA 723  
Db 531 tctgcaactgatactctctcttctcgcacgcgtcgtcgtlaatgttcatggaacacaa 590  
QY 724 TCTGCAATTGGCTCTCTGCAATCATCTGTTGTTATATCAGCGATAGTCTTGGAGCACCA 783  
Db 591 aatacaggca-g-g-gg-tc-catagattgcaacctcaagttctccaccacaacctggt 644  
QY 784 AAGTCAGGGAAGATGTGATGTCATGTAATGCTTCCTTGACGTTTCCGTATGATGATATT 843  
Db 645 actgg-gaagac-ctgc-tcaaatctgtgtcttattcttgccttcaatcagcggtcc 701  
QY 844 CCTGGTGGATCTCTTCATGAAAGATCTGTCTCTGCTTGTGCTTGTGATCCCACTCC 903  
Db 702 tcatactactgtgtgttacgycctgatatcttaagactcaagagcgttcgactgtat 761  
QY 904 TCATCATCATGTTCTGCTTACACCCCTGATGATCCTGCGCCTGAAGAGTGTCCGCTCCTGT 963  
Db 762 cgggtcccaagaagaagagcaggaatctgcgacgagatcaaccgagatggtggtgctg 821  
QY 964 CTGGCTCCCGAGAGAAGACCGAATCTCCGCCGATCACCAAGCTGTGTGTTAGTAG 1023  
Db 822 tggctgtatttactcgtctgtggaaccccatccacatctacgtcatcatcaagaagcgtga 881  
QY 1024 TTGCACTCTTCATCATCTGTGTGACCCCAATTCACATCTTTATCCTGGTGAAGCTCTGG 1083  
Db 882 tcaagattccagaaaacacatttcaagaccgtttcctgycacttctgcatlgtgtgtt 941  
QY 1084 GAAGCACTCCACACAGCACAGCTGCCCTCTCCAGCTATATTCTGTATTTGCCCTGGGT 1143  
Db 942 acacgaacagctgacctgaatccagttctttagccttctcgtgatatgaacttcaagcgtat 1001  
QY 1144 ATACCAACAGCAGCCTGAATCCTGTCTCTATGCTTCTTGTGATGAAACTCAAGCGGT 1203  
Db 1002 gcttcagagagttctgcatccc 1023  
QY 1204 GTTTTAGGGACTTCTGCTTCCC 1225

RESULT 6  
ID Q89222 standard; cDNA; 1618 BP.  
AC Q89222;  
DI 20-OCT-1995 (first entry)  
DE Rat mu opioid receptor cDNA.  
KW Mu opioid receptor; MOR-1; gene therapy; diagnostic; ss.  
OS Rattus sp.  
FH Key Location/Qualifiers  
FT CDS 214..1410  
FT /tag= a  
PN WO9507983-A.  
PD 23-MAR-1995.  
PF 13-SEP-1994; U10358.  
PR 13-SEP-1993; US-120601.  
PA (INDV ) UNIV INDIANA FOUND.  
PI Yu L;  
DR WPI; 95-131351/17.  
DR P-PSDB; R71964.  
PT New nucleic acid encoding new human mu opioid receptor - and  
PT related vectors, transformed cells, antibodies etc., useful in  
PT diagnosis, treatment and drug screening.  
PS Disclosure; Page 190-194; 266pp; English.  
CC A 365 bp fragment of the mouse delta opioid receptor was used to  
CC screen a rat brain cDNA library under low stringency conditions.  
CC One positive clone included the sequence given in Q89222, encoding a  
CC mu opioid receptor, MOR-1 (R71964). MOR-1 was stably expressed in  
SQ transfect CHO cells. Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T;



QY 1024 TTGCAGTCTTCATCATCTGTGGACCCCATTCACATCTTTATCCTGGTGAGGCTCTGG 1083  
Db 1130 tcaagattccagaacacacattcagaccggtttccctggcaacttctgcatctgttggtt 1189  
QY 1084 GAAGCACTCCACAGACAGCTGCCCTCTCCAGCTATTATTCTGTATTGCTTGGGT 1143  
Db 1190 acaagcaagctgacctgaatcagttctttacgacctccctgagatgaanaactcaagcat 1249  
QY 1144 ATACCAACAGCAGCCTGAATCTCTCTATGACCTTTCTGGATGAATAACTCAAGCGGT 1203  
Db 1250 gcttcagagagttctgcatccc 1271  
QY 1204 GTTTTAGGGACTTCTGCTTCCC 1225

RESULT 8  
ID Q56705 standard; cDNA; 1981 BP.  
AC Q56705;  
DT 15-SEP-1994 (first entry)  
DE Partial sequence of the murine mu-receptor clone DOR-2  
KW (MOR-1, MOR-1alpha)  
OS Opioid receptor; morphine; opiate; ss.  
PN Mus musculus.  
PN W09404552-A.  
PD 03-MAR-1994.  
PF 13-AUG-1993; U07665.  
PR 13-AUG-1992; US-929200.  
PA (REGC ) UNIV CALIFORNIA.  
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;  
DR WPI; 94-083099/10.  
PT DNA encoding opioid receptors and antibodies against this  
PT receptor - used to express and locate these receptors, and screen  
PT cpds. for opioid (ant)agonist activity  
PS Example; Fig 9; 74pp; English.  
CC A cDNA library prepd. from mouse brain was probed using DOR-1 (see  
CC Q56704) as a probe. One clone was recovered and sequenced. This  
CC clone, designated DOR-2, represented a new gene. DOR-2 hybridised  
CC to a different pattern of neurons than did DOR-1 and showed greater  
CC labeling of the striatum. The identity of DOR-2 (mMOR-1) as that of  
CC a mu receptor was confirmed.  
SQ Sequence 1981 BP; 499 A; 549 C; 436 G; 496 T;

Query Match 21.9%; Score 309; DB 10; Length 1981;  
Best Local Similarity 70.6%; Pred. No. 1.96e-203;  
Matches 606; Conservative 0; Mismatches 243; Indels 9; Gaps 8;

Db 465 catcatggccctctattctatcggtgtgtagtgggacctttggaacttcctgtcat 524  
QY 368 CATCACCGCTGTCTACTCTGTGTATTGTGTGGCTTAGTGGCAATTCTCTGTGTCAT 427  
Db 525 gtatgtgatttgaagatatcaanaatgaagactggccacaacatctacatttcaacct 584  
QY 428 GTTTGTATCATCCGATACAGAGATGAAGACCGCAACACATCTACATATTAACT 487  
Db 585 tgctctggcagatggccttagccactagcagcgtgacctttcagagtggttaactactgat 644  
QY 488 GGCCTTGGCAGATGCTTGGTTACTACCACTATGCCCTTTCAAGAGTGCTGTCTACTGAT 547  
Db 645 gggaacgtggcccttggaaacatccctctgcaacatgaagttagcagcgtacatgacctg 704  
QY 548 GAATTCCTTGGCCTTTGGAGATGTGCTATGCAAGATTGTCAATTCCATTGACTACTACAA 607  
Db 705 catgttaccagtatcttcaacctctgcaacatgaagttagcagcgtacatgacctgctg 764  
QY 608 CATGTTACCAGCATATTCACTTGACCATGATGATGTGACCGCTACATGCTGTGTG 667  
Db 765 ccaccggtcaagcctgagttccgtaacccccgaatatgccaatatgtcaatgtctg 824  
QY 668 CCACCTGTGAAGCTTTGGACTTCCGAACACCTTTGAAAGCAAGATCATCAACATCTG 727  
Db 825 caactgatacctctctctctgcaattgtgtctgcccgtaatgttcatggaacacaaata 884

QY 728 CATTTGGCTCCTGGCATCATCTGTGTATATCAGCGATAGTCCCTGGAGGACCAAGT 787  
Db 885 caagca-g-g-gg-tc-catatatgcaacccctcaagttctctcatccacatggtactg 938  
QY 788 CAGGGAAGATGTGATGTCAATTGAATGCTCCTTGACGTTTCTTGATGATGAATATCTCG 847  
Db 939 g-gagaac-ctgc-tcaaatctgtgtctctcatcttcgcccttcatcatgcccggccat 995  
QY 848 GTGGATCTCTTCATGAGATCTGTCTCTGCTTTGGCTTTGTGATCCAGTCTCAT 907  
Db 996 catcactgtgttattatgactgatgatcttacagctcaagagtgtccgcatgtgtcgg 1055  
QY 908 CATCATTTGTCTGTACACCTGATGATCCTGGCCTGAAGAGTGTCCGGCTCCTGTCTG 967  
Db 1056 ctccaaagaaaggaagcaacctgcygagatcaacccgagtggtgtgtgtgtgtgc 1115  
QY 968 CTCCGAGAGAAGGACCGAAATCTCCGCCGCAACCAAGCTGGTGTCTGTAGTTGC 1027  
Db 1116 tgattattgtctgtgagcccccatccacatctatgtcatcatcaagcactgatcac 1175  
QY 1028 AGTCTTCATCATCTGTGTGACCCCCCATTCACATCTTATCTCTGTGAGGCTCTGGAAG 1087  
Db 1176 gattccagaacocatttccagactgtttctctggcacttctgcatgacctgtgtgtacac 1235  
QY 1088 CACCTCCACAGACAGCAGCTGCCCTCTCCAGCTATTATTCTGTATGTGCTTGGTTATAC 1147  
Db 1236 aacagctgtctgaacccagttctttatgcgttctcgtgatgaanaactcaacgatgtt 1295  
QY 1148 CAACAGCAGCCTGAATCTCTGTCTATGCTTCTGTGATGAATAACTCAAGCGGTGTT 1207  
Db 1296 tagagagttctgcatccc 1313  
QY 1208 TAGGACTTCTGCTTCCC 1225

RESULT 9  
ID Q56700 standard; cDNA; 1821 BP.  
AC Q56700;  
DT 15-SEP-1994 (first entry)  
DE Sequence of murine delta opioid receptor in the DOR-1 cDNA clone.  
KW Opioid receptor; morphine; opiate; ss.  
OS Mus musculus.

FH Key Location/Qualifiers  
FT CDS 29..1139  
FT /\*tag= a

PN W09404552-A.  
PD 03-MAR-1994.  
PF 13-AUG-1993; U07665.  
PR 13-AUG-1992; US-929200.  
PA (REGC ) UNIV CALIFORNIA.  
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;  
DR WPI; 94-083099/10.  
DR P-PSDB; R48629.  
PT DNA encoding opioid receptors and antibodies against this  
PT receptor - used to express and locate these receptors, and screen  
PT cpds. for opioid (ant)agonist activity  
PS Claim 1; Fig 5; 74pp; English.  
CC A cDNA library was constructed using mRNA isolated from the NG109-15  
CC cell line. A single clone, named the DOR-1 clone was isolated.  
CC Comparisons with known sequences in GenBank showed highest homology  
CC between DOR-1 and the G-protein-coupled somatostatin receptor. Other  
CC features of the DOR-1 clone AA sequence deduced from the cDNA  
CC sequence include 3 consensus glycosylation sites at residues 18 and  
CC 33 (predicted to be in the extracellular N-terminal domain), and at  
CC residue 310 (close to the C-terminus and predicted to be  
CC intracellular). Phosphokinase C consensus sites are present within  
CC predicted intracellular domains, at residues 242,255, 344 & 352.  
CC Seven putative membrane-spanning regions were identified. The DOR-1  
CC clone produces a delta receptor with a predicted mol. wt. of 40,558  
CC kaitons prior to post-translational modifications.  
SQ Sequence 1821 BP; 339 A; 559 C; 541 G; 382 T;

Query Match 20.6%; Score 291; DB 10; Length 1821;



Best Local Similarity 70.8%; Pred. No. 5.67e-190;  
Matches 597; Conservative 0; Mismatches 234; Indels 12; Gaps 8;

Db	181	catcacgcgcgtctactcgctgtgtgcygcaagtgggctctctgggcaacgtgtctcat	240
QY	368	CATCACCGCTGTCTACTCTGTGTAATTTGTGTGGGCTTAGTGGCAATTCCTGTGICAT	427
Db	241	gtttgcatcgtccggtacacaaattgaagaccgcaacaacatctacatcttcaatct	300
QY	428	GTTTGTATCATCCGATACAGAGATGAAGACCGCAACCAACATCTACATATTTAACT	487
Db	301	ggcttggctgtagtgcgtgcaaccagcagctgcccctccagagcgccaaagtactgat	360
QY	488	GCGTTGGCAGATGCTTTGGTACTACCACTATGCCCTTTTCAGAGTGTCTACTTGAT	547
Db	361	cgaaacgtggccglttggcgagcgtgtgcaagcgtgtgtctccattgactactacaa	420
QY	548	GAATTTCTTGCCCTTTTGAGATGTGCTATGCAAGATTGTCAATTGCCATTGACTACTACAA	607
Db	421	catgttcaactagcatcttcaaccctcaacatgatgagcgtgagccgtacattgtgtctg	480
QY	608	CATGTTTACCAAGCATATTCACCTTGACCATGATGAGTGTGACCGCTACATGCTGTGTG	667
Db	481	ccatccgtgcaaaagccctggaactccgggacacaccagccaagccaagctgtatcaata	540
QY	668	CCACCCTGTGAAGCTTTGACTTCGGAACACCTTTGAAAGCAAGATCATCAACATCTG	727
Db	541	catctggtcttggcttcaaggtgtcgsggtcccaatcatgtgtcatgagtgaccacaac	600
QY	728	CATTTGGCTCCTGGCATCATCTGTGTGTAATACAGCGATAGTCTTGGAGGACCAAAAGT	787
Db	601	ccggatgtgtgcagtggt-at-gcatgtccc---agttccccaagtcceagctgtaactg	654
QY	788	CAGGGAAGATGTGATGTCATTTGAATGCTCTCTTGACGTTTCTTGATGATGAATATTCCTG	847
Db	655	g-gaca-ctgtg-accaaagatctgctgttctctcttgccttgcctgtgtgagcagatccat	711
QY	848	GTGGATCTCTTCATGAAGATCTGTGTCTCTGCTTTGGCTTTGTGATCCAGTCTCTCAT	907
Db	712	catcacggtgtgtctatgacctcatgtactgagcctgagcagcgtgtctgtctgtccg	771
QY	908	CATCATTTGTCTGTACACCCCTGATGATCCTGCGCTGAAGAGTGTCCGGCTCTCTCTG	967
Db	772	ttccaaggaagacgcagcctgcggcgcatcaacgcgcgatgtgtgtgtgtgtgtg	831
QY	968	CTCCCGAGAGAAGGACGAATCTCCGCCGCATCAACCAAGCTGGTGTGTAGTAGTTGC	1027
Db	832	cgccctcgt	891
QY	1028	AGTCTTCATCATCTGTGGAACCCCATTCACATCTTTATCTGTGT--GGAGGCTCTGGGA	1085
Db	892	catcaatcgcgcgaccactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	951
QY	1086	-AGCAACTCCACAGACAGACTGCCCTCTCCAGCTAATTATTCTGTATTGGCTTGGGTTA	1144
Db	952	cgccaacagcagcctcaacccggttctctacgcttctctgtgaagagaacttcaagcgtg	1011
QY	1145	TACCAACAGCAGCCTGAATCCTGTCTCTATGCTTTCGATGAAAACCTCAAGCGGTG	1204
Db	1012	ctt 1014	
QY	1205	TTF 1207	

RESULT 10  
ID 075927 standard; DNA; 2272 BP.  
AC 075927;  
DT 17-AUG-1995 (first entry)  
DE Mouse delta opioid receptor MOR1 cDNA.  
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;  
transmembrane domain; somatostatin; receptor; human; expression vector;  
truncate; chimaeric; assay; probe; ss.  
OS Mus musculus.

Key Location/Qualifiers  
CDS 12..1130

FT /\*tag= a  
FT /product= mouse delta opioid receptor  
PN W09428132-A.  
PD 08-DEC-1994.  
PE 20-MAY-1994; U05747.  
PR 20-MAY-1993; US-066296.  
PR 30-JUL-1993; US-100694.  
PR 05-NOV-1993; US-147592.  
PA (ARCH-) ARCH DEV CORP.  
PI Bell GI, Reisine T, Yasuda K;  
DR WPI; 95-022804/03.  
DR P-PSDB; R67670.  
PT Polynucleotides and peptides derived from opioid receptor  
PT polypeptides - for use in therapeutic compositions and in  
PT screening assays for useful drug substances.  
PS Claim 6; page 215-221; 300pp; English.  
CC The nucleotide sequence of the novel mouse delta opioid receptor gene  
CC MOR1. The gene was isolated from a mouse brain cDNA library using a  
CC fragment (amplified from the cDNA library with primers 075929-30) as a  
CC probe. The primers are based on the conserved sequences present in the  
CC second and third transmembrane domains of somatostatin (SRIF) receptor  
CC subtypes SS1R1, SS1R2 and SS1R3. The 1.3 kb EcoRI-SacI fragment from the  
CC mouse delta opioid receptor clone, lambda ms1-2, was subcloned into the  
CC CMV promoter-based expression vector pCMV-6c. The resultant construct  
CC pCMV-ms1-2 was transfected into COS-1 cells for protein production. The  
CC gene encoding the opioid receptor can be used to produce complete,  
CC truncated or chimaeric opioid receptor proteins. The opioid receptors  
CC thus produced are useful for the development of novel assays designed to  
CC select or improve substances, capable of interacting with the opioid  
CC receptor proteins, for use in diagnosis, drug design and therapeutic  
CC applications.  
SQ Sequence 2272 BP; 485 A; 665 C; 650 G; 472 T;

Query Match 20.6%; Score 291; DB 13; Length 2272;  
Best Local Similarity 70.8%; Pred. No. 5.67e-190;  
Matches 597; Conservative 0; Mismatches 234; Indels 12; Gaps 8;

Db	164	catcacgcgcgtctactcgcgtgtgtgcygcaagtgggctctctgggcaacgtgtctcat	223
QY	368	CATCACCGCTGTCTACTCTGTGTATTTGTGTGGGCTTAGTGGCAATTCCTGTGTCAT	427
Db	224	gtttgcatcgtccggtlaacaaatltgaagaccgccaacaacatctacatcttcaatct	283
QY	428	GTTTGTATCATFCGATACACGAAGATGAAGACCGCAACCAACATCTACATATTTAACT	487
Db	284	ggcttggctgtagtgcgtgcaaccagcagctgccccttccagagcgccaagtaactgat	343
QY	488	GGCTTTGGCAGATGCTTTGGTTACTACCACTATGCCCTTTCAAGAGTGTGTCTACTTGAT	547
Db	344	ggaaacgtggccgtttggcgagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	403
QY	548	GAATTTCTTGCCCTTTTGAGATGTGCTATGCAAGATGTGATTTCCATTGACTACTACAA	607
Db	404	catgttcaactagcatcttcaaccctcaacatgatgagcgtgagccgtacattgtgtctg	463
QY	608	CATGTTTACCAAGCATATTCACCTTGACCATGATGAGTGAACCGCTACATTCGTGTGTG	667
Db	464	ccatcctgtcaaaagccctggaactccggacacccagccaagccaagctgtatcaataatg	523
QY	668	CCACCCTGTGAAGCTTTGGAAGCTTCGGAACACCTTTGAAGCAAGATCATCAACATCTG	727
Db	524	catctgggtctgtgctcaggt	583
QY	728	CATTTGGCTCCTGGCATCATCTGTGTATATACAGCGATAGTCTTGAGGACCAAGT	787
Db	584	ccggatgtgtgcagtggt-at-gcatgtccc---agttccccaagtcceagctgtaactg	637
QY	788	CAGGGAAGATGTGATGTCAATGAATGCTCTTGACGTTTCTTGATGATGAATATTCCTG	847
Db	638	g-gaca-ctgtg-accaaagatctgcgtgttctctcttgccttgcctgtgtgtgtgtgtgt	694



QY 848 GTGGGATCTCTTCATGAGATCTGTGCTCTTGCCTTTTGATCCAGTCCCTCAT 907  
Db 695 catcacggtgtgtctatggccctcaatgtctactgagccctgcgaagcgltgcgtgtccgg 754  
QY 908 CATCATGTGCTGCTACACCCCTGATGATCCTGCGCCTGAAGAGTGTCCGGCTCTGTGG 967  
Db 755 ttccaaggagaaggacgcgcctgcggcgcatcacgagcgatggtgtgtgtgtgg 814  
QY 968 CTCGCCGAGAGAGGACCGAAATCTCCGCCGATCACCAAGCTGTGCTGTAGTAGTTC 1027  
Db 815 cgccctcgtgtgtgtgtgcggcccatccacatcttgcgtcatcgtctgtgagcgctgtgga 874  
QY 1028 AGTCTTCATCATCTGTGGACCCCATTCACATCTTATCCTGGT--GGAGGCTCTGGGA 1085  
Db 875 catcaatcgcgcgacccaactgtgtggtgcccgaactgcacctgtgcattgagctgggcta 934  
QY 1086 -AGCACCTCCACAGACAGACGCTGCCCTCTCCAGCTATTATTCTGTATTGCTTGGGTTA 1144  
Db 935 cgccaacagcagccctcaacccggttctctactacgacctcctggaagagaactcaagcgctg 994  
QY 1145 TACCAACAGACGACCGCTGAATCCTGTCTCTATGCTTCTTGATGAAACCTTCAAGCGGTG 1204  
Db 995 ctt 997  
QY 1205 TTT 1207

RESULT 11  
ID Q89226 standard; cDNA; 1610 BP.  
AC Q89226;  
DT 20-OCT-1995 (first entry)  
DE Human mu opioid receptor cDNA.  
KW Mu opioid receptor; MOR; gene therapy; diagnostic; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 239..1441  
FT /\*tag= a  
PN WO9507983-A.  
PD 23-MAR-1995.  
PF 13-SEP-1994; U10358.  
PR 13-SEP-1993; US-120601.  
PA (INDV ) UNIV INDIANA FOUND.  
PI Yu L;  
DR WPI; 95-131351/17.  
DR P-PSDB; R71966.  
PT New nucleic acid encoding new human mu opioid receptor - and  
PT related vectors, transformed cells, antibodies etc., useful in  
PT diagnosis, treatment and drug screening.  
PS Claim 5; Page 208-210; 266pp; English.  
CC A cDNA library constructed from human caudate nucleus mRNA was  
CC screened with rat mu opioid receptor cDNA under conditions of  
CC low stringency. One positive clone included the sequence given in  
CC Q89226, encoding a mu opioid receptor MOR (R71964). The cDNA  
CC is used for prodn. of recombinant MOR, in gene therapy, etc.  
SQ Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T;

Query Match 20.5%; Score 289; DB 14; Length 1610;  
Best Local Similarity 70.0%; Pred. No. 1.77e-188;  
Matches 601; Conservative 0; Mismatches 246; Indels 11; Gaps 10;

Db 455 atcatggccctctactccatcggtggtggtggtctctcgaaacttcctgtcatg 514  
QY 369 ATGACCGCTGTCTACTCTGTGTAATTGTGTGGCTTAGTGGCAATTCTGTGTCATG 428  
Db 515 tatgtattgtcagatataccaagatgaagactgccaaccaatctacatttcaacctt 574  
QY 429 TTTGTTCATCATCCGATACAGAGATGAAGACCGCAACCACTACTATTTAACTG 488  
Db 575 gctctggcagatgacctagccaacagttaccctgccccttccaagagtgtgaattacaatg 634  
QY 489 GCTTTGGCAGATGCTTGGTACTACCACTATGCCCTTTCAGAGTGTGCTACTTGATG 548  
Db 635 ggaacatggccatttggaaaccattcttgcagaagatgatatctcatagattactataac 694

QY 549 AATTCCTGGCCCTTTGGAGATGTGCTATGCAAGATGTGCATTTCCATTGACTACTACAAC 608  
Db 695 atgtcacccagcatattcaaccctctgcaccatgagtgttgatcgatacatgtcagtcgc 754  
QY 609 ATGTTTACCAGCATATTCACCTTGACCATGATGATGTGGACCGCTACATTGCTGTGTGC 668  
Db 755 caccctgtcaaggcccttagatttccgtactccccgaaatgccaaaatlatcaatgtctgc 814  
QY 669 CACCCGTGAAGCCTTTGGACTTCGGAACACCTTTGAAGCAAGATCATCAATCTGC 728  
Db 815 aactggatcctctctcagccatgtgtcttctctgtaatgttcattgctacacaanaatac 874  
QY 729 ATTTGGCTCCTGGCATCATCTGTTGTTATATCAGCGATAGTCCCTTGAGGCAACCAAGTC 788  
Db 875 aggcaaggt-tccatag-attgta--cac-taacattctc-tcatccaacctggtactg 928  
QY 789 AGGGAAGATGTGATGTTCATTGAATGCTCCTTGAGATTCTCTGATGATGAATATTCCTGG 848  
Db 929 -gaaac-ctgc-tgaagatctgtgttctcatcttcgaccttcattatgtcagtcctac 985  
QY 849 TGGATCTCTTCATGAAGATCTGTGTCTCTGCTTTCCTTTTGGATCCAGTCTCATC 908  
Db 986 attacgltgtgtctatgtagctgatgatcttgcgcctcaagagtgtccgaatgctctgc 1045  
QY 909 ATCATGTCTGTCAACACCCCTGATGATCTGTGCTCTGCTTTCCTTTGATCCAGTCTCATC 968  
Db 1046 tccaaagaaaggacaggaaatcttcgaagatacaacagatggtgtgtgtgtgct 1105  
QY 969 TCCCGAGAGAGGAGCCGAATCTCCGCCGATCACCAAGCTGTGTGTAGTAGTTGCA 1028  
Db 1106 gtgtcatcgtctgtgtgacctcccatcaattacgtcatcatcaagcctgtgtaca 1165  
QY 1029 GTCTTCATCATCTGTTGGACCCCATTCACATCTTATCCTGTGTGAGGCTCTGGGAAGC 1088  
Db 1166 atcccagaactac-gttccagactgttcttggcaacttctgcattgtcttagttacac 1224  
QY 1089 ACCTCCACAGACACAGCTGCCCTCTCCAGCTATT-ATTCTGTATTGCCCTGGTTATAC 1147  
Db 1225 aaacagctgcctcaacccagtcctttagtcatlcttgatgaaacttcaacgatgctt 1284  
QY 1148 CAACAGCAGGCTGAATCCTGTCTCTATGCCCTTCTGTGATGAAAACTTCAAGCGGTGTT 1207  
Db 1285 cagagagttctgtatccc 1302  
QY 1208 TAGGACTTCTGCTTCCC 1225

RESULT 12  
ID Q93102 standard; cDNA; 2160 BP.  
AC Q93102;  
DT 11-DEC-1995 (first entry)  
DE Human mu opiate receptor cDNA.  
KW Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;  
KW drug abuse; analgesic; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 213..1415  
FT /\*tag= a  
PN WO9520667-A1.  
PD 03-AUG-1995.  
PF 30-JAN-1995; U01144.  
PR 28-JAN-1994; US-188275.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (USSH ) US SEC DEPT HEALTH.  
PI Johnson PS, Persico AM, Uhl G, Wang J;  
DR WPI; 95-275452/36.  
DR P-PSDB; R76780.  
PT New DNA encoding human mu opiate receptor - used esp. for screening  
PT cpds. for activity as opiate agonists or antagonists  
PS Claim 4; Page 24-25; 49pp; English.  
CC hMOR cDNA was obt'd. from a human cerebral cortical cDNA library  
CC screened with fragments of a rat mu opiate receptor. Cloned hMOR



Db 739 catcacggtgtgtatgtgcccctcatgtactgtgcccgtgcagcgtgtgtgtctgtccgg 798  
QY 908 CATCATGTGTGTGTACACCCCTGATGATCCTGCGCCTGAAGAGTGTCCGGCTCCTGTCTGG 967  
Db 799 ttccaaggagaagaccgcagcctgcggcgcatcaagcgcatgtgtgtgtgtgtgtgg 858  
QY 968 CTCCCGAGAGAGACCGAATCTCCGCGCATCAACCAAGCTGTGTGTGTGTGTGTGTGC 1027  
Db 859 cgccttcgtga 918  
QY 1028 AGTCTTCATCATGT 1085  
Db 919 catcaatcgcgcgaccactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 978  
QY 1086 -AGCACCTCCACAGACAGCTGCCCTTCACGCTATTTCTGTGTGTGTGTGTGTGTGT 1144  
Db 979 cggcaacagcagcctcaaccggttctctacgccttcctgagcagaactcaagcgtg 1038  
QY 1145 TACCAACAGCAGCCTGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1204  
Db 1039 ctt 1041  
QY 1205 TTT 1207

RESULT 14  
ID Q56703 standard; DNA; 829 BP.  
AC Q56703:  
DT 15-SEP-1994 (first entry)  
DE Partial sequence of the human mu opioid receptor  
DE genomic clone H20 (MORA).  
KW Opioid receptor; morphine; opiate; ss.  
OS Homo sapiens.  
PN WO9404552-A.  
PD 03-MAR-1994.  
PF 13-AUG-1993; U07665.  
PR 13-AUG-1992; US-929200.  
PA (REGC ) UNIV CALIFORNIA.  
PI Edwards RH, Evans CJ, Kaufman D, Keith DE,  
DR WPI; 94-083099/10.  
PT DNA encoding opioid receptors and antibodies against this  
PT receptor - used to express and locate these receptors, and screen  
PT cpds. for opioid (antagonist activity  
PS Example; Fig 8c; 74pp; English.  
CC To isolate opiate receptor genomic clones, 300,000 human genomic  
CC clones and a similar number of mouse genomic clones were probed  
CC with the 1.1 kb mouse delta opioid receptor clone DOR-1 Pst/XbaI  
CC fragment. One mouse clone and three human genomic clones were  
CC isolated. The 3 human clones had very different EcoRI patterns  
CC which indicated that three different genes were represented by the  
CC human genomic clones which were designated H3, H14 and H20. H20 maps  
CC to chromosome 6. It encodes the human mu receptor. In addition, H20  
CC appears to contain a CACACA marker (Q56704) which provides a means  
CC to track the inheritance of this gene.  
SQ Sequence 829 BP; 182 A; 205 C; 134 G; 214 T;

Query Match 16.3%; Score 230; DB 10; Length 829;  
Best Local Similarity 62.8%; Pred. No. 1.45e-144;  
Matches 493; Conservative 0; Mismatches 279; Indels 13; Gaps 12;  
Db 16 gatacacaagatgaagactgccaccacacatctacatttcaacctgtgtctg-cagatg 74  
QY 442 GATACACGAAGATGAAGACCGCAACCACTCTACATATTAACTGCTTTGGCAGATG 501  
Db 75 ccttagccacagtlaccctgccttcagagtggtgaattacctaattggaacatggccat 134  
QY 502 CTTTGTACTACCACTATGCCCCCTTCAAGTGTCTCTACTTGATGAATTTCTTGCCCTT 561  
Db 135 ttggaacatctcttgcaagatagtgtctccatagattactataacatgttcaaccagca 194  
QY 562 TTGGAGATGTGCTATGCAAGATTGTCTATTTCCATTGACTACTACAACATGTTTACCAGCA 621  
Db 195 tattcaccctctgcaccatgagtgtttgatcgatacatgtgcagtlgtccaccctgtcaag 254

QY 622 TATTACCTTGACCATGATGAGTGTGACCCCTACATTTGCTGTGTGTGCCACCCCTGAAAG 681  
Db 255 ccttagatttcogtactccnn 314  
QY 682 CTTTGACTTCCGAACACCTTTGAAGCAAGATCATCAACATCTGCATTGGCTCCTGG 741  
Db 315 nngt-tcc 373  
QY 742 CATCATCTGTGTGTATATACGCGATAGTCTTTGGAGGCACCAAGTACGGAAGATGTGG 801  
Db 374 atag-attgta--aac-taacattctc-tcatccaacctggtactgg-gaaaac-ctgc- 425  
QY 802 ATGTCAATTGAATGCTCCTTGACAGTTTCTGTGATGATGAATATTCCTGGTGGGATCTCTCA 861  
Db 426 tgaagatctgtgttttcaatcttgcccttcattatgccaagtgtcattacattacgtgtgt 485  
QY 862 TGAAGATCTGTGTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 921  
Db 486 atggaatgatgtatcttgccctcaagagtgtccgcagtgtctctgtgtccaaagaaag 545  
QY 922 ACACCCGTATGATCCTTGCGCCCTGAAGAGTGTCCGGCTCTGTGTGTGTGTGTGTGTGT 981  
Db 546 acaggaatcttcgaagatcaccaagagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 605  
QY 982 ACCGAATCTCCGCCGCATCACCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1041  
Db 606 gctggaatccattcacattacgtcatcattaaagcctgtgttacatccagaacta 665  
QY 1042 GTTGAACCCCATTCACATCTTATCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1101  
Db 666 c-gttccaagactgttcttggaactctgtcattgtgtctgtgtgtgtgtgtgtgtgtgtgt 724  
QY 1102 CAGCTGCCCTCTCCAGCTAAT-ATTCTGTATTTGCCCTTGGGTTATACCAACAGCAGCTG 1160  
Db 725 aaccagtccttlatgcaattctgtgatgaacttcca-cgatgcttcagagagttctgt 783  
QY 1161 AATCCTGTCTCTATGCTTCTGTGATGAAGAACTCAAGCGGTGTTTAGGAGCTTCTGC 1220  
Db 784 atccc 788  
QY 1221 TTCCC 1225

RESULT 15  
ID Q89233 standard; cDNA; 1567 BP.  
AC Q89233:  
DT 20-OCT-1995 (first entry)  
DE Rat opioid receptor cDNA.  
KW Opioid receptor; MOR-1; gene therapy; diagnostic; ss.  
OS Rattus sp.  
FH Key  
FT CDS location/Qualifiers  
FT CDS 173..1276  
FT /\*tag= a  
PN WO9507983-A.  
PD 23-MAR-1995.  
PF 13-SEP-1994; U10358.  
PR 13-SEP-1993; US-120601.  
PA (INDV ) UNIV INDIANA FOUNDD.  
PI Xu L;  
DR WPI; 95-131351/17.  
DR P-PSDB; R71968.  
PT New nucleic acid encoding new human mu opioid receptor - and  
PT related vectors, transformed cells, antibodies etc., useful in  
PT diagnosis, treatment and drug screening.  
PS Example 9; Page 218-222; 266pp; English.  
CC The cDNA given in Q89233 was isolated from a rat brain library by  
CC low stringency hybridization with rat mu opioid receptor cDNA  
CC (Q89222). The clone encoded a 367-amino acid protein (R71968)  
CC that showed high homology with mu, kappa and delta opioid receptors  
CC but lacked affinity for their ligands, suggesting it to be  
CC a novel member of the opioid receptor family.  
SQ Sequence 1567 BP; 313 A; 440 C; 402 G; 412 T;

